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OM protein - protein search, using sw model

Run on: August 13, 2003, 09:39:40 ; Search time 83 Seconds
(without alignments)
15.299 Million cell updates/sec

Title: US-10-056-052A-29
Perfect score: 44
Sequence: 1 HQYLSSYT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	8	AAE29276	Anti-Clfa monoclon
2	44	100.0	112	AAE29266	S. aureus Clfa spe
3	44	100.0	112	AAE29268	S. aureus Clfa spe
4	44	100.0	112	AAE29270	S. aureus Clfa spe
5	39	88.6	112	AAE29270	Fc receptor humani
6	39	88.6	112	AAE29270	Mab 022 VK chain.
7	39	88.6	112	AAE29264	S. aureus Clfa spe
8	39	88.6	113	AAE29215	LL2 Mab VK region.
9	39	88.6	113	AAE29217	Humanised LL2 Mab

10	39	88.6	113	18	AAW27695	Variable kappa cha
11	39	88.6	115	18	AAW27697	Variable kappa cha
12	39	88.6	263	20	AAW90226	Anti-B7.2 monospec
13	39	88.6	268	20	AAW90228	Anti-B7.1/anti-B7.
14	39	88.6	268	20	AAW90222	Anti-B7.2 monospec
15	39	88.6	273	20	AAW90224	Anti-B7.1/anti-B7.
16	39	88.6	301	18	AAW11507	Single chain, huma
17	39	88.6	301	20	AAW73217	Multispecific sing
18	39	88.6	301	22	AAW85454	Single chain human
19	39	88.6	301	22	AAW61959	Single chain human
20	39	88.6	352	20	AAW06272	Anti-Fc gamma rece
21	39	88.6	553	18	AAW11508	Single chain anti-
22	39	88.6	553	20	AAW73223	H22-anti-CEA antib
23	39	88.6	553	22	AAW85455	Bispecific single
24	39	88.6	553	22	AAW61960	Bispecific single
25	39	88.6	556	20	AAW90218	Bispecific tetra
26	39	88.6	580	20	AAW90217	Bispecific tetra
27	36	81.8	112	23	ABG70739	Variable chain of
28	36	81.8	238	23	ABG70744	Mouse/human chimer
29	35	79.5	272	23	ABG31024	Synthetic mouse fu
30	34	77.3	86	22	AAW99674	Human excretory re
31	34	77.3	86	22	AAW42489	Human kidney relat
32	34	77.3	468	21	AAW75167	Neisseria meningit
33	34	77.3	543	22	ABB71263	Drosophila melanog
34	33	75.0	330	22	ABB57984	Drosophila melanog
35	33	75.0	554	18	AAW01824	Manduca sexta larv
36	33	75.0	554	21	AAW07183	Manduca sexta gut
37	33	75.0	554	24	ABP72619	Manduca sexta chit
38	33	75.0	921	21	AAW32297	Corn polycomb prot
39	33	75.0	931	23	AAO14529	Protein of Mez1 (M
40	33	75.0	1369	22	ABB60839	Drosophila melanog
41	33	75.0	2308	15	AAW52580	RPTP-beta amino ac
42	32	72.7	52	23	ABP03502	Human OREF protein
43	32	72.7	210	21	AAW34736	Human secreted pro
44	32	72.7	226	24	ABJ19065	Pathogen specific
45	32	72.7	235	22	AAU33959	Staphylococcus aur

ALIGNMENTS

RESULT 1
AAE29276
ID AAE29276 standard; peptide; 8 AA.

XX

AC AAE29276;

XX

DT 27-JAN-2003 (first entry)

XX

DE Anti-Clfa monoclonal antibody variable light chain CDR3.

XX

KW Clumping factor A; Clfa; fibrinogen; fibrin; Clf40; Clf33; N3 protein;

KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;

KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy;

KW complementarity determining region; CDR.

XX

OS Unidentified.

XX

PN WO200272600-A2.

XX

PD 19-SEP-2002.

XX

PF 28-JAN-2002; 2002WO-US02296.

XX

PR 26-JAN-2001; 2001US-264072P.

PR 12-MAR-2001; 2001US-274611P.

PR 18-JUN-2001; 2001US-298413P.

PR 30-JUL-2001; 2001US-308116P.

XX

PA (INHI-) INHIBITEX INC.

XX

PI Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX

DR WPI; 2002-759834/82.

XX New anti-clumping factor A (ClfA) monoclonal antibody, useful for

PT treating or preventing Staphylococcus aureus infection e.g. wound

PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis

PT in a human or animal

XX

PS Claim 31; Page 55; 80pp; English.

XX

CC The invention relates to monoclonal antibody which binds the clumping

CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA

CC monoclonal antibody is useful for treating or preventing S. aureus

CC infection in a human or animal, and for inhibiting the binding of

CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment

CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3

CC protein is useful for inducing an immunological response in a human or

CC animal. These staphylococcal infections include wound infections, sepsis,

CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The

CC present sequence is an anti-ClfA monoclonal antibody variable light chain

CC complementarity determining region (CDR).

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 44; DB 23; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8

Db 1 HQYLSSYT 8

RESULT 2

AAE29266

ID AAE29266 standard; Protein; 112 AA.

XX

AC AAE29266;

XX

DT 27-JAN-2003 (first entry)

XX

DE S. aureus ClfA specific monoclonal antibody 12-9VLA-1 protein.

XX

KW Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;

KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;

KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

XX

OS Staphylococcus aureus.

XX

FH Key Location/Qualifiers

FT Region 24..40

FT /note= "CDR1"

FT Region 56..62

FT /note= "CDR2"

FT Region 95..102

FT /note= "CDR3"

PN WO200272600-A2.

XX

PD 19-SEP-2002.

XX

PF 28-JAN-2002; 2002WO-US02296.

XX

PR 26-JAN-2001; 2001US-264072P.

PR 12-MAR-2001; 2001US-274611P.

PR 18-JUN-2001; 2001US-298413P.

PR 30-JUL-2001; 2001US-308116P.

XX

PA (INHIT-) INHIBITEX INC.

XX

PI Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX

DR WPI; 2002-759834/82.

DR N-PSDB; AAD46865.

XX

PT New anti-clumping factor A (ClfA) monoclonal antibody, useful for

PT treating or preventing Staphylococcus aureus infection e.g. wound

PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis

PT in a human or animal

XX

PS Claim 11; Page 35; 80pp; English.

XX

CC The invention relates to monoclonal antibody which binds the clumping

CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA

CC monoclonal antibody is useful for treating or preventing S. aureus

CC infection in a human or animal, and for inhibiting the binding of

CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment

CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3

CC protein is useful for inducing an immunological response in a human or

CC animal. These staphylococcal infections include wound infections, sepsis,

CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The

CC present sequence is Staphylococcus aureus ClfA specific monoclonal

CC antibody 12-9VLA-1 (variable light sequence) protein.

XX

SQ Sequence 112 AA;

Query Match 100.0%; Score 44; DB 23; Length 112;

Best Local Similarity 100.0%; Pred. No. 0.28;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8

Db 95 HQYLSSYT 102

RESULT 3

AAE29268

ID AAE29268 standard; Protein; 112 AA.

XX

AC AAE29268;

XX

DT 27-JAN-2003 (first entry)

XX

DE S. aureus ClfA specific monoclonal antibody 35-220VLD-4 protein.

XX

KW Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;

KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;

KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

XX

OS Staphylococcus aureus.

XX

FH Key Location/Qualifiers

FT Region 24..40

FT /note= "CDR1"

FT Region 56..62

FT /note= "CDR2"

FT Region 95..102

FT /note= "CDR3"

PN WO200272600-A2.

XX

PD 19-SEP-2002.

XX

PF 28-JAN-2002; 2002WO-US02296.

XX

PR 26-JAN-2001; 2001US-264072P.

PR 12-MAR-2001; 2001US-274611P.

PR 18-JUN-2001; 2001US-298413P.

PR 30-JUL-2001; 2001US-308116P.

XX

PA (INHIT-) INHIBITEX INC.

XX

PI Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX

DR WPI; 2002-759834/82.

DR N-PSDB; AAD46867.

PT New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis
PT in a human or animal -
XX
PS Claim 11; Page 37; 80pp; English.
XX
CC The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 35-220VLD-4 (variable light sequence) protein.

Sequence 112 AA;
Query Match 100.0%; Score 44; DB 23; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HQYLSSYT 8
| | | | |
Db 95 HQYLSSYT 102

RESULT 4
AAE29270
ID AAE29270 standard; Protein; 112 AA.
XX
AC AAE29270;
XX
DT 27-JAN-2003 (first entry)
XX
DE S. aureus ClfA specific monoclonal antibody 12-9VL-Hu protein.
XX
KW Clumping factor A; ClfA; fibrinogen; fibrin; Clf40; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.
XX Staphylococcus aureus.
OS
XX
FH Key Location/Qualifiers
Region 24..40
/note= "CDR1"
Region 56..62
/note= "CDR2"
Region 95..102
/note= "CDR3"
WO200272600-A2.
XX
PN 19-SEP-2002.
XX
PD 28-JAN-2002; 2002WO-US02296.
XX
PF 26-JAN-2001; 2001US-264072P.
PR 12-MAR-2001; 2001US-274611P.
PR 18-JUN-2001; 2001US-298413P.
PR 30-JUL-2001; 2001US-308116P.
XX
PA (INHIBITEX INC.
XX
XX Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;
PI WPI; 2002-759834/82.
DR N-PSDB; AAD46869.
XX
PT New anti-clumping factor A (ClfA) monoclonal antibody, useful for

PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis
PT in a human or animal -
XX
PS Claim 11; Page 42; 80pp; English.
XX
CC The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 12-9VL-Hu (humanised variable light sequence) protein.
XX
SQ Sequence 112 AA;
Query Match 100.0%; Score 44; DB 23; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HQYLSSYT 8
| | | | |
Db 95 HQYLSSYT 102

RESULT 5
AAR54932
ID AAR54932 standard; peptide; 112 AA.
XX
AC AAR54932;
XX
DT 25-MAR-2003 (updated)
DT 19-OCT-1994 (first entry)
XX
DE Fc receptor humanized VK chain 022 HuVK.
XX
KW Fc receptor; FcR; humanized antibody; hAb; IgG; cancer; allergy;
KW autoimmune disease; heteroantibody; bifunctional antibody;
KW immunotoxin; CDR; complementarity determining region; VH;
KW heavy chain variable region; VK; kappa chain variable region;
KW mononuclear phagocyte; PCR; polymerase chain reaction; primer;
KW site-directed mutagenesis; HuVK; monoclonal antibody; MAb.
XX
OS Homo sapiens; Mus sp.
XX
PN WO9410332-A1.
XX
PD 11-MAY-1994.
XX
PF 04-NOV-1993; 93WO-US10384.
XX
PR 04-NOV-1992; 92GB-0023377.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Carr FJ, Harris WJ, Tempest PR;
XX
DR WPI; 1994-167486/20.
XX
PT New humanised antibodies to Fc receptors - used for diagnosis or
PT for treatment of e.g. cancer, allergies and infectious and
PT auto-immune diseases
XX
PS Disclosure; Page 16; 36pp; English.
XX
CC Humanized antibodies (hAbs) for IgG Fc receptors on human phagocytes
CC comprise the CDR of mouse monoclonal antibody 22 (from hybridoma
CC 022WCL-1), VH chains from human Igs NEWM or KOL, and VK chains from
CC Ig REI. Sequences are provided for mouse 022 VH (AAR54931),

CC humanized NEWM-based VH (022 NMVH, AAR54929), humanized KOL-
CC based VH (022 KLVH, AAR54930), mouse 022 VK (AAR54933) and humanized
CC REI- based VK (022 HuVK, AAR54932). During hab production, VH and VK
CC cDNAs were PCR amplified using primers given in AAQ65378-87.
CC Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was performed using
CC oligos AAQ65388-89. The habs can be used in heteroantibody,
CC bifunctional antibody and immunotoxin production.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 112 AA;

Query Match 88.6%; Score 39; DB 15; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
| | | | | : |
Db 95 HQYLSSWT 102

RESULT 6
AAR54933
AAR54933 standard; peptide; 112 AA.

AC AAR54933;

DT 25-MAR-2003 (updated)
DT 19-OCT-1994 (first entry)

DE MAB 022 VK chain.

XX
KW Fc receptor; FcR; humanized antibody; hAb; IgG; cancer; allergy;
KW autoimmune disease; heteroantibody; bifunctional antibody;
KW immunotoxin; CDR; complementarity determining region; VH;
KW heavy chain variable region; VK; kappa chain variable region;
KW mononuclear phagocyte; PCR; polymerase chain reaction; primer;
KW site-directed mutagenesis; monoclonal antibody; MAb.

XX Mus sp.

XX WO9410332-A1.

XX 11-MAY-1994.

PF 04-NOV-1993; 93WO-US10384.

PR 04-NOV-1992; 92GB-0023377.

XX (MEDA-) MEDAREX INC.

XX Carr FJ, Harris WJ, Tempest PR;

XX WPI; 1994-167486/20.

XX
PT New humanised antibodies to Fc receptors - used for diagnosis or
PT for treatment of e.g. cancer, allergies and infectious and
PT auto-immune diseases

PS Disclosure; Page 23; 36pp; English.

XX
CC Humanized antibodies (hAbs) for IgG Fc receptors on human phagocytes
CC comprise the CDR of mouse monoclonal antibody 22 (from hybridoma
CC 022WCL-1), VH chains from human Igs NEWM or KOL, and VK chains from
CC Ig REI. Sequences are provided for mouse 022 VH (AAR54931),
CC humanized NEWM-based VH (022 NMVH, AAR54929), humanized KOL-
CC based VH (022 KLVH, AAR54930), mouse 022 VK (AAR54933) and humanized
CC REI- based VK (022 HuVK, AAR54932). During hab production, VH and VK
CC cDNAs were PCR amplified using primers given in AAQ65378-87.
CC Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was performed using
CC oligos AAQ65388-89. The habs can be used in heteroantibody,
CC bifunctional antibody and immunotoxin production.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 112 AA;

Query Match

Best Local Similarity 88.6%; Score 39; DB 15; Length 112;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8

| | | | | : |

Db 95 HQYLSSWT 102

RESULT 7

AAE29264

ID AAE29264 standard; Protein; 112 AA.

XX

AC AAE29264;

XX

DT 27-JAN-2003 (first entry)

XX

DE S. aureus ClfA specific monoclonal antibody 13-2VLA-1 protein.

XX

KW Clumping factor A; ClfA; fibrinogen; fibrin; Clf33; N3 protein;
KW immunological; staphylococcal infection; impetigo; pneumonia; furuncle;
KW septic arthritis; sepsis; endocarditis; antibacterial; wound; therapy.

XX Staphylococcus aureus.

XX

FH Key Location/Qualifiers

FT Region 24...40

FT /note= "CDR1"

FT Region 56...62

FT /note= "CDR2"

FT Region 95...102

FT /note= "CDR3"

XX

PN WO200272600-A2.

XX

PD 19-SEP-2002.

XX

PF 28-JAN-2002; 2002WO-US02296.

XX

PR 26-JAN-2001; 2001US-264072P.

PR 12-MAR-2001; 2001US-274611P.

PR 18-JUN-2001; 2001US-298413P.

PR 30-JUL-2001; 2001US-308116P.

XX

PA (INH-) INHIBITEX INC.

XX

PI Patti JM, Hutchins JT, Domanski P, Patel P, Hall A;

XX WPI; 2002-759834/82.

DR N-PSDB; AAD46863.

XX

PT New anti-clumping factor A (ClfA) monoclonal antibody, useful for
PT treating or preventing Staphylococcus aureus infection e.g. wound
PT infections, impetigo, furuncles, pneumonia, septic arthritis or sepsis
PT in a human or animal

XX

PS Claim 11; Page 34; 80pp; English.

XX

CC The invention relates to monoclonal antibody which binds the clumping
CC factor A (ClfA) protein from Staphylococcus aureus. The anti-ClfA
CC monoclonal antibody is useful for treating or preventing S. aureus
CC infection in a human or animal, and for inhibiting the binding of
CC staphylococcal bacteria to fibrinogen or fibrin. The immunogenic fragment
CC S. aureus Clf40 protein, S. aureus Clf33 protein, or the S. aureus N3
CC protein is useful for inducing an immunological response in a human or
CC animal. These staphylococcal infections include wound infections, sepsis,
CC impetigo, furuncles, pneumonia, septic arthritis or endocarditis. The
CC present sequence is Staphylococcus aureus ClfA specific monoclonal
CC antibody 13-2VLA-1 (variable light sequence) protein.

XX SQ Sequence 112 AA;

Query Match 88.6%; Score 39; DB 23; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HQYLSSYT 8
Db 95 HQYLSSHT 102

RESULT 8
AAR92215
ID AAR92215 standard; Protein; 113 AA.
XX
AC AAR92215;
XX
DT 28-MAY-1996 (first entry)
XX
LL2 MAb VK region.

Humanised antibody; monoclonal antibody; MAb; LL2; B-cell lymphoma;
leukaemia; therapy; diagnosis; complementarity determining region;
CDR; antibody engineering.

Mus musculus.
Key Location/Qualifiers
Region 24..40
FT /label= CDR1
FT /note= "claim 6, page 44"
FT Region 56..62
FT /label= CDR2
FT /note= "claim 7, page 44"
FT Region 95..103
FT /label= CDR3
FT /note= "claim 8, page 44"
XX
PN WO9604925-A1.
XX
PD 22-FEB-1996.
XX
PF 11-AUG-1995; 95WO-US09641.
XX
PR 12-AUG-1994; 94US-0289576.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen H, Leung S;
XX
WPI; 1996-139454/14.
N-PSDB; AAT15802.

Chimeric and humanised LL2 antibodies - used to produce conjugates
for the therapy and diagnosis of B-cell lymphoma(s) and
leukaemia(s).

Claim 5; Page 35-36; 70pp; English.

The complementarity determining regions (CDRs) of mouse monoclonal
antibody (MAb) LL2 VK (AAR92215) and VH (AAR92216) regions were
recombinantly linked to the framework sequences of human VK and VH
regions, respectively, to give humanised LL2 VK (AAR92217) and VH
(AAR92218). These were subsequently linked, respectively, to human
kappa and IgG1 constant regions. A humanised MAb was obtd. that
retained the B-lymphoma and leukaemia cell targeting and
internalisation characteristics of the parental LL2 MAb, and which
exhibited a lowered HAMA reaction. It can be linked to e.g. a
cytostatic agent for therapeutic appln.

Query Match 88.6%; Score 39; DB 17; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.8;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

RESULT 9
AAR92217
ID AAR92217 standard; Protein; 113 AA.
XX
AC AAR92217;
XX
DT 28-MAY-1996 (first entry)
XX
DE Humanised LL2 MAb VK region.

Humanised antibody; monoclonal antibody; MAb; LL2; B-cell lymphoma;
leukaemia; therapy; diagnosis; complementarity determining region;
CDR; antibody engineering.

Synthetic.
Key Location/Qualifiers
Region 24..40
FT /label= CDR1
FT Region 56..62
FT /label= CDR2
FT Region 95..103
FT /label= CDR3
XX
PN WO9604925-A1.
XX
PD 22-FEB-1996.
XX
PF 11-AUG-1995; 95WO-US09641.
XX
PR 12-AUG-1994; 94US-0289576.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen H, Leung S;
XX
WPI; 1996-139454/14.
N-PSDB; AAT15803.

Chimeric and humanised LL2 antibodies - used to produce conjugates
for the therapy and diagnosis of B-cell lymphoma(s) and
leukaemia(s).

Claim 5; Page 38; 70pp; English.

The complementarity determining regions (CDRs) of mouse monoclonal
antibody (MAb) LL2 VK (AAR92215) and VH (AAR92216) regions were
recombinantly linked to the framework sequences of human VK and VH
regions, respectively, to give humanised LL2 VK (AAR92217) and VH
(AAR92218). These were subsequently linked, respectively, to human
kappa and IgG1 constant regions. A humanised MAb was obtd. that
retained the B-lymphoma and leukaemia cell targeting and
internalisation characteristics of the parental LL2 MAb, and which
exhibited a lowered HAMA reaction. It can be linked to e.g. a
cytostatic agent for therapeutic appln.

Sequence 113 AA;

Query Match 88.6%; Score 39; DB 17; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

RESULT 10
AAW27695
ID AAW27695 standard; Protein; 113 AA.
XX
AC AAW27695;
XX
DT 14-APR-1998 (first entry)
XX
DE Variable kappa chain of MAb LL2.
XX
KW Variable kappa chain; B cell; monoclonal antibody; MAB; LL2;
KW B cell lymphoma; lymphocytic leukaemia cell; murine;
KW diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
KW chronic lymphocytic leukaemia.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 18..20
FT /note= "potential N-linked glycosylation site"
FT Region 24..40
FT /note= "complementarity determining region 1"
FT Region 56..62
FT /note= "complementarity determining region 2"
FT Region 95..102
FT /note= "complementarity determining region 3"
XX
PN WO9734632-A1.
XX
PD 25-SEP-1997.
XX
PF 19-MAR-1997; 97WO-US04196.
XX
PR 20-MAR-1996; 96US-0013709.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen H, Leung S, Qu Z;
XX
DR WPI; 1997-479995/44.
DR N-PSDB; AAT88128.
XX
PT Monoclonal antibody engineered to contain glycosylation site - in
PT non-Fc constant heavy or light chain region, useful to diagnose or
PT treat B cell malignancies, e.g. non-Hodgkins lymphoma
XX
PS Example 3; Fig 4A; 88pp; English.
CC
CC The present sequence is the variable kappa chain of the
CC B cell specific monoclonal antibody (MAB) LL2, which contains an
CC engineered tri-peptide N-glycan acceptor sequence. LL2 is a highly
CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
CC murine MAB. The MAB can be used to diagnose or treat B
CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
CC lymphocytic leukaemia. The glycosylation site allows a label or
CC therapeutic agent of increased size to be conjugated to the
CC carbohydrate moiety, without affecting the MAB's binding affinity
XX or specificity.
SQ Sequence 113 AA;
Query Match 88.6%; Score 39; DB 18; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HQYLSSYT 8
Db 95 HQYLSSWT 102
RESULT 11
AAW27695
ID AAW27695 standard; Protein; 113 AA.
XX
AC AAW27695;
XX
DT 14-APR-1998 (first entry)
XX
DE Variable kappa chain of MAB LL2.
XX
KW Variable kappa chain; B cell; monoclonal antibody; MAB; LL2;
KW B cell lymphoma; lymphocytic leukaemia cell; murine;
KW diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
KW chronic lymphocytic leukaemia.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 18..20
FT /note= "potential N-linked glycosylation site"
FT Region 24..40
FT /note= "complementarity determining region 1"
FT Region 56..62
FT /note= "complementarity determining region 2"
FT Region 95..102
FT /note= "complementarity determining region 3"
XX
PN WO9734632-A1.
XX
PD 25-SEP-1997.
XX
PF 19-MAR-1997; 97WO-US04196.
XX
PR 20-MAR-1996; 96US-0013709.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen H, Leung S, Qu Z;
XX
DR WPI; 1997-479995/44.
DR N-PSDB; AAT88128.
XX
PT Monoclonal antibody engineered to contain glycosylation site - in
PT non-Fc constant heavy or light chain region, useful to diagnose or
PT treat B cell malignancies, e.g. non-Hodgkins lymphoma
XX
PS Example 3; Fig 4A; 88pp; English.
CC
CC The present sequence is the variable kappa chain of the
CC B cell specific monoclonal antibody (MAB) LL2, which contains an
CC engineered tri-peptide N-glycan acceptor sequence. LL2 is a highly
CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
CC murine MAB. The MAB can be used to diagnose or treat B
CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
CC lymphocytic leukaemia. The glycosylation site allows a label or
CC therapeutic agent of increased size to be conjugated to the
CC carbohydrate moiety, without affecting the MAB's binding affinity
XX or specificity.
SQ Sequence 113 AA;
Query Match 88.6%; Score 39; DB 18; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

AAW27697
ID AAW27697 standard; Protein; 115 AA.
XX
AC AAW27697;
XX
DT 14-APR-1998 (first entry)
XX
DE Variable kappa chain of MAB hLL2.
XX
KW Variable kappa chain; B cell; monoclonal antibody; MAB; hLL2;
KW B cell lymphoma; lymphocytic leukaemia cell; murine; humanised;
KW diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
KW chronic lymphocytic leukaemia.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 24..40
FT /note= "complementarity determining region 1"
FT Region 56..62
FT /note= "complementarity determining region 2"
FT Region 95..102
FT /note= "complementarity determining region 3"
XX
PN WO9734632-A1.
XX
PD 25-SEP-1997.
XX
PF 19-MAR-1997; 97WO-US04196.
XX
PR 20-MAR-1996; 96US-0013709.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen H, Leung S, Qu Z;
XX
DR WPI; 1997-479995/44.
DR N-PSDB; AAT88130.
XX
PT Monoclonal antibody engineered to contain glycosylation site - in
PT non-Fc constant heavy or light chain region, useful to diagnose or
PT treat B cell malignancies, e.g. non-Hodgkins lymphoma
XX
PS Example 3; Fig 5A; 88pp; English.
XX
CC The present sequence is the variable kappa chain of the
CC B cell specific monoclonal antibody (MAB) hLL2. hLL2 is a highly
CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
CC humanised murine MAB. The MAB can be used to diagnose or treat B
CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
CC lymphocytic leukaemia.
SQ Sequence 115 AA;
Query Match 88.6%; Score 39; DB 18; Length 115;
Best Local Similarity 87.5%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HQYLSSYT 8
Db 95 HQYLSSWT 102
RESULT 12
AAW27697
ID AAW27697 standard; Protein; 263 AA.
XX
AC AAW27697;
XX
DT 10-MAY-1999 (first entry)
XX
DE Anti-B7.2 monospecific triabody 1G10.

XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
KW CD86; T cell activation; inhibitor; graft versus host disease;
KW transplant rejection; allograft rejection; autoimmune disease;
KW allergy; therapy; human; triabody; antibody; 1G10.
XX
OS Chimeric - Mus sp.
OS Chimeric - synthetic.

XX Key Location/Qualifiers
FH Peptide 1..24 /note= "pelB signal peptide"
FT Region 25..144
FT Peptide 145..257 /note= "anti B7.2 MAb VH region"
FT Peptide 258..263 /note= "anti B7.2 MAb VL region"
FT Peptide /note= "His6 tag"

XX WO9858965-A2.

PD 30-DEC-1998.

XX 22-JUN-1998; 98WO-EP03791.

XX 20-JUN-1997; 97EP-0870092.

XX (INNO-) INNOGENETICS NV.

XX Bosman A, Buyse M, Lorre K, Sablon E;

XX WPI; 1999-105615/09.

DR N-PSDB; AAX01660.

XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection

XX Example 7.3; Fig 34; 182pp; English.

XX This polypeptide comprises a 1G10 monospecific triabody composed
CC of the VH region of anti-B7.2 monoclonal antibody (MAb) 1G10
CC joined to the VL region of 1G10. A triabody is a mono- a bi- or
CC a trispecific molecule recognising simulataneously e.g. two B7.2
CC and one B7.1 molecules. It has a rigid structure that prevents
CC simultaneous binding to the 3 targets. Each antigen-binding site
CC is formed by pairing of one VH and one VL domain from the same or
CC from two different polypeptides. The invention relates to novel
CC molecules, including triabodies, which can cross-link and/or
CC cross-react with the costimulatory molecules B7.1 and B7.2 expressed
CC on professional antigen-presenting cells, leading to the inhibition
CC of antigen-specific T cell activation. Methods are provided for
CC the production of such B7-binding molecules, and for their use in
CC the treatment or prevention of diseases of the immune system, in
CC particular graft rejection, graft versus host disease, allergy and
CC autoimmune diseases (claimed).

XX Sequence 263 AA;

Query Match 88.6%; Score 39; DB 20; Length 263;
Best Local Similarity 87.5%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 239 HQYLSSWT 246

RESULT 13
AAW90228
ID AAW90228 standard; Protein; 268 AA.

XX AAW90228;
AC
XX

DT 10-MAY-1999 (first entry)
XX Anti-B7.1/anti-B7.2 bispecific triabody II.
DE B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX CD86; T cell activation; inhibitor; graft versus host disease;
KW transplant rejection; allograft rejection; autoimmune disease;
KW allergy; therapy; human; triabody; antibody; B7-24; 1G10.
XX

OS Chimeric - Mus sp.
OS Chimeric - synthetic.
XX Key Location/Qualifiers
FH Peptide 1..39 /note= "g3p signal peptide"
FT Region 40..155
FT Peptide /note= "anti B7.1 MAb VH region"
FT Peptide 156..268 /note= "anti B7.2 MAb VL region"

XX WO9858965-A2.

PD 30-DEC-1998.

XX 22-JUN-1998; 98WO-EP03791.

XX 20-JUN-1997; 97EP-0870092.

XX (INNO-) INNOGENETICS NV.

XX Bosman A, Buyse M, Lorre K, Sablon E;

XX WPI; 1999-105615/09.

DR N-PSDB; AAX01662.

XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection

XX Example 7.3; Fig 38; 182pp; English.

XX This polypeptide comprises a bispecific triabody composed of the VH
CC region of anti-B7.1 monoclonal antibody (MAb) B7-24 joined to the
CC VL region of anti-B7.2 MAb 1G10. A triabody is a mono- a bi- or
CC a trispecific molecule recognising simulataneously e.g. two B7.2
CC and one B7.1 molecules. It has a rigid structure that prevents
CC simultaneous binding to the 3 targets. Each antigen-binding site
CC is formed by pairing of one VH and one VL domain from the same or
CC from two different polypeptides. The invention relates to novel
CC molecules, including triabodies, which can cross-link and/or
CC cross-react with the costimulatory molecules B7.1 and B7.2 expressed
CC on professional antigen-presenting cells, leading to the inhibition
CC of antigen-specific T cell activation. Methods are provided for
CC the production of such B7-binding molecules, and for their use in
CC the treatment or prevention of diseases of the immune system, in
CC particular graft rejection, graft versus host disease, allergy and
CC autoimmune diseases (claimed).

XX Sequence 268 AA;

Query Match 88.6%; Score 39; DB 20; Length 268;
Best Local Similarity 87.5%; Pred. No. 7.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 250 HQYLSSWT 257

RESULT 14
AAW90222
ID AAW90222 standard; Protein; 268 AA.

XX AAW90222;
AC

```
XX 10-MAY-1999 (first entry)
XX Anti-B7.2 monospecific diabody 1G-10.
DE B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX CD86; T cell activation; inhibitor; graft versus host disease;
KW transplant rejection; allograft rejection; autoimmune disease;
KW allergy; therapy; human; diabody; antibody; 1G-10.
XX
OS Chimeric - Mus sp.
OS Chimeric - synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT /note= "pelB signal peptide"
FT Region 25..144
FT /note= "anti B7.2 MAb VH region"
FT Peptide 145..149
FT /note= "G4S flexible linker"
FT Region 150..262
FT /note= "anti B7.2 MAb VL region"
FT Peptide 263..268
FT /note= "His6 tag"
XX
XX WO9858965-A2.
XX 30-DEC-1998.
XX
XX 22-JUN-1998; 98WO-EP03791.
XX
XX 20-JUN-1997; 97EP-0870092.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Bosman A, Buyse M, Lorre K, Sablon E;
XX
XX WPI; 1999-105615/09.
XX N-PSDB; AAX01656.
XX
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection
XX
XX Example 7.2; Fig 26; 182pp; English.
XX
XX This polypeptide comprises a 1G-10 monospecific diabody composed
XX of the VH region of anti-B7.2 monoclonal antibody (MAB) 1G-10
XX joined via a short, flexible linker to the VL region of 1G-10.
XX Mono- or bispecific bivalent molecules are generated by shortening
XX the flexible linker sequence between the VH and VL of the anti-B7.1
XX scFv B7-24, the anti-B7.2 scFv 1G10 and the scFv molecule with
XX dual specificity for B7.1 and B7.2 (B7.12) to 5-10 residues, and
XX for bispecific molecules by cross-pairing the VH and VL domains
XX from the 2 scFvs with different antigen recognition (B7.1/B7.2 and
XX B7.12/B7.12). The invention relates to novel molecules, including
XX diabodies, which can cross-link and/or cross-react with the
XX costimulatory molecules B7.1 and B7.2 expressed on professional
XX antigen-presenting cells, leading to the inhibition of antigen-
XX specific T cell activation. Methods are provided for the
XX production of such B7-binding molecules, and for their use in the
XX treatment or prevention of diseases of the immune system, in
XX particular graft rejection, graft versus host disease, allergy and
XX autoimmune diseases (claimed).
XX
XX Sequence 268 AA;
XX
XX Query Match 88.6%; Score 39; DB 20; Length 268;
XX Best Local Similarity 87.5%; Pred. NO. 7.2;
XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HQYLSSYT 8
XX |||||:|
XX Db 244 HQYLSSWT 251
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RESULT 15
AAW90224
ID AAW90224 standard; Protein; 273 AA.
XX
XX AAW90224;
AC
XX
XX 10-MAY-1999 (first entry)
XX
XX Anti-B7.1/anti-B7.2 bispecific diabody II.
DE
XX
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
KW CD86; T cell activation; inhibitor; graft versus host disease;
KW transplant rejection; allograft rejection; autoimmune disease;
KW allergy; therapy; human; diabody; antibody; B7-24; 1G10.
XX
OS Chimeric - Mus sp.
OS Chimeric - synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..39
FT /note= "g3p signal peptide"
FT Region 40..155
FT /note= "anti B7.1 MAb VH region"
FT Peptide 156..160
FT /note= "G4S flexible linker"
FT Region 161..273
FT /note= "anti B7.2 MAb VL region"
FT Misc-difference 21
FT /note= "encoded by TCA"
XX
XX WO9858965-A2.
XX
XX 30-DEC-1998.
XX
XX 22-JUN-1998; 98WO-EP03791.
XX
XX 20-JUN-1997; 97EP-0870092.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Bosman A, Buyse M, Lorre K, Sablon E;
XX
XX WPI; 1999-105615/09.
XX N-PSDB; AAX01658.
XX
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection
XX
XX Example 7.2; Fig 30; 182pp; English.
XX
XX This polypeptide comprises a bispecific diabody composed of the VH
XX region of anti-B7.1 monoclonal antibody (MAB) B7-24 joined via a
XX short, flexible linker to the VL region of anti-B7.2 MAB 1G10.
XX Mono- or bispecific bivalent molecules are generated by shortening
XX the flexible linker sequence between the VH and VL of the anti-B7.1
XX scFv B7-24, the anti-B7.2 scFv 1G10 and the scFv molecule with
XX dual specificity for B7.1 and B7.2 (B7.12) to 5-10 residues, and
XX for bispecific molecules by cross-pairing the VH and VL domains
XX from the 2 scFvs with different antigen recognition (B7.1/B7.2 and
XX B7.12/B7.12). The invention relates to novel molecules, including
XX diabodies, which can cross-link and/or cross-react with the
XX costimulatory molecules B7.1 and B7.2 expressed on professional
XX antigen-presenting cells, leading to the inhibition of antigen-
XX specific T cell activation. Methods are provided for the
XX production of such B7-binding molecules, and for their use in the
XX treatment or prevention of diseases of the immune system, in
XX particular graft rejection, graft versus host disease, allergy and
XX autoimmune diseases (claimed).
XX
XX Sequence 273 AA;
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Query Match 88.6%; Score 39; DB 20; Length 273;
Best Local Similarity 87.5%; Pred. NO. 7.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||||:|
Db 255 HQYLSSWT 262

Search completed: August 13, 2003, 09:45:14
Job time : 85 secs

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OM protein - protein search, using sw model

Run on: August 13, 2003, 09:18:10 ; Search time 16 Seconds
(without alignments)
21.155 Million cell updates/sec

Title: US-10-056-052A-29
Perfect score: 44
Sequence: 1 HQYLSSYT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	88.6	112	4	US-08-435-516-4
2	39	88.6	112	4	US-08-435-516-28
3	39	88.6	113	1	US-08-690-102A-2
4	39	88.6	113	1	US-08-690-102A-6
5	39	88.6	113	3	US-09-127-902-2
6	39	88.6	113	3	US-09-127-902-6
7	39	88.6	113	3	US-09-155-107-2
8	39	88.6	113	3	US-09-155-107-6
9	39	88.6	113	3	US-09-155-107-20
10	39	88.6	113	5	PCT-US95-09641-2
11	39	88.6	113	5	PCT-US95-09641-6
12	39	88.6	301	2	US-08-661-052-14
13	39	88.6	301	3	US-09-188-082-14
14	39	88.6	301	4	US-09-364-088-14
15	39	88.6	301	4	US-09-102-716-14
16	39	88.6	553	2	US-08-661-052-16
17	39	88.6	553	3	US-09-188-082-16
18	39	88.6	553	4	US-09-364-088-16
19	39	88.6	553	4	US-09-102-716-16
20	33	75.0	554	2	US-08-524-051-2
21	33	75.0	554	3	US-09-052-778-16
22	33	75.0	902	4	US-09-699-266A-12
23	33	75.0	921	4	US-09-699-266A-9
24	32	72.7	87	4	US-09-328-352-7319
25	31	70.5	313	4	US-09-328-352-7621
26	31	70.5	390	4	US-09-134-001C-3112
27	31	70.5	588	1	US-07-903-466-3

28	31	70.5	588	5	PCT-US93-05794-3	Sequence 3, Appli
29	30	68.2	162	4	US-09-522-217-2	Sequence 2, Appli
30	30	68.2	308	4	US-09-252-991A-20925	Sequence 20925, A
31	30	68.2	357	4	US-09-574-942-4	Sequence 4, Appli
32	30	68.2	414	1	US-08-255-471-9	Sequence 9, Appli
33	30	68.2	459	3	US-09-071-709-1	Sequence 1, Appli
34	30	68.2	519	4	US-09-522-217-85	Sequence 85, Appli
35	30	68.2	655	4	US-09-245-808-1	Sequence 1, Appli
36	30	68.2	655	4	US-09-767-594-1	Sequence 9, Appli
37	30	68.2	667	3	US-09-071-709-9	Sequence 9, Appli
38	30	68.2	814	4	US-09-107-532A-5510	Sequence 5510, Ap
39	30	68.2	829	4	US-09-252-991A-27150	Sequence 27150, A
40	30	68.2	873	3	US-09-187-331-6	Sequence 6, Appli
41	30	68.2	873	4	US-09-470-946-6	Sequence 6, Appli
42	30	68.2	873	4	US-09-438-906-2	Sequence 2, Appli
43	30	68.2	873	4	US-09-438-906-4	Sequence 4, Appli
44	30	68.2	925	2	US-08-392-946-1	Sequence 1, Appli
45	30	68.2	925	2	US-08-504-169-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-435-516-4
; Sequence 4, Application US/08435516
; Patent No. 6500931
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
; FILING DATE: 04-NOV-1992; -02-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-435-516-4

Query Match 88.6%; Score 39; DB 4; Length 112;
Best Local Similarity 87.5%; Pred. No. 0.92;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

RESULT 2
US-08-435-516-28
; Sequence 28, Application US/08435516

; Patent No. 6500931
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
; TITLE OF INVENTION: IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
; FILING DATE: 04-NOV-1992; -02-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-435-516-28

Query Match 88.6%; Score 39; DB 4; Length 112;
Best Local Similarity 87.5%; Pred. No. 0.92;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

RESULT 3
US-08-690-102A-2
; Sequence 2, Application US/08690102A
; Patent No. 5789554
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-On
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,102A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 424
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-690-102A-6

Query Match 88.6%; Score 39; DB 1; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8

; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-690-102A-2

Query Match 88.6%; Score 39; DB 1; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

RESULT 4
US-08-690-102A-6
; Sequence 6, Application US/08690102A
; Patent No. 5789554
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-On
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,102A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/463/IMIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-690-102A-6

Query Match 88.6%; Score 39; DB 1; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8

RESULT 8
US-09-155-107-6
; Sequence 6, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: OU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-155-107-6

Query Match 88.6%; Score 39; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1-HQYLSSYT 8
|||||:|
Db 95 HQYLSSWT 102

RESULT 9
US-09-155-107-20
; Sequence 20, Application US/09155107
; Patent No. 6254868
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: OU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/0879
; CURRENT APPLICATION NUMBER: US/09/155,107
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: US 60/013,709
; EARLIER FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-155-107-20

Query Match 88.6%; Score 39; DB 3; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1-HQYLSSYT 8
|||||:|
Db 95 HQYLSSWT 102

RESULT 10
PCT-US95-09641-2
; Sequence 2, Application PC/TUS9509641
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09641
; FILING DATE: 11-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09641-2

Query Match 88.6%; Score 39; DB 5; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1-HQYLSSYT 8
|||||:|
Db 95 HQYLSSWT 102

RESULT 11
PCT-US95-09641-6
; Sequence 6, Application PC/TUS9509641
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
; NUMBER OF SEQUENCES: 21
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09641
; FILING DATE: 11-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,576
; FILING DATE: 12-AUG-1994
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09641-6

Query Match 88.6%; Score 39; DB 5; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.93;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1-HQYLSSYT 8
|||||:|
Db 95 HQYLSSWT 102

RESULT 12
US-08-661-052-14
; Sequence 14, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein

;; APPLICANT: Robert Graziano
;; APPLICANT: Chezian Somasundaram
;; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
;; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD
;; STREET: 60 State Street, Suite 510
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109-1875
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/661,052
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/484,172
;; FILING DATE: 07-JUNE-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Arnold, Beth E.
;; REGISTRATION NUMBER: 35,430
;; REFERENCE/DOCKET NUMBER: MXI-043CP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)227-5941
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 301 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-661-052-14

Query Match 88.6%; Score 39; DB 2; Length 301;
Best Local Similarity 87.5%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
| | | | | : |
Db 249 HQYLSSWT 256

RESULT 13
-09-188-082-14
Sequence 14, Application US/09188082
Patent No. 6270765
;; GENERAL INFORMATION:
;; APPLICANT: Yashwant M. Deo
;; APPLICANT: Joel Goldstein
;; APPLICANT: Robert Graziano
;; APPLICANT: Chezian Somasundaram
;; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
;; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD
;; STREET: 60 State Street, Suite 510
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109-1875
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/188,082

;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/661,052
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Arnold, Beth E.
;; REGISTRATION NUMBER: 35,430
;; REFERENCE/DOCKET NUMBER: MXI-043CP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)227-5941
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 301 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-188-082-14

Query Match 88.6%; Score 39; DB 3; Length 301;
Best Local Similarity 87.5%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
| | | | | : |
Db 249 HQYLSSWT 256

RESULT 14
US-09-364-088-14
Sequence 14, Application US/09364088
Patent No. 6365161
;; GENERAL INFORMATION:
;; APPLICANT: Yashwant M. Deo, et al.
;; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
;; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD, LLP
;; STREET: 28 State Street, 24th Floor
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/364,088
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/188,082
;; FILING DATE: 07-JUNE-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/484,172
;; FILING DATE: 07-JUNE-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Remillard, Jane E.
;; REGISTRATION NUMBER: 38,872
;; REFERENCE/DOCKET NUMBER: MXI-043CP2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-7414
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 301 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-364-088-14

Query Match 88.6%; Score 39; DB 4; Length 301;
Best Local Similarity 87.5%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
| | | | | : |
Db 249 HQYLSSWT 256

RESULT 15

US-09-102-716-14
; Sequence 14, Application US/09102716
; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; Joel Goldstein
; Robert Graziano
; Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-102-716-14

Query Match 88.6%; Score 39; DB 4; Length 301;
Best Local Similarity 87.5%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
| | | | | : |
Db 249 HQYLSSWT 256

Search completed: August 13, 2003, 09:39:56
Job time : 17 secs

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OM protein - protein search, using sw model

Run on: August 13, 2003, 09:37:35 ; Search time 24 Seconds
(without alignments)
43.668 Million cell updates/sec

Title: US-10-056-052A-29
Perfect score: 44
Sequence: 1 HQYLSSYT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues
Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : , Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	112	15	US-10-056-052-10 Sequence 10, Appl
2	44	100.0	112	15	US-10-056-052-14 Sequence 14, Appl
3	44	100.0	112	15	US-10-056-052-18 Sequence 18, Appl
4	39	88.6	112	12	US-10-229-335-4 Sequence 4, Appli
5	39	88.6	112	12	US-10-229-335-28 Sequence 28, Appl
6	39	88.6	112	15	US-10-056-052-6 Sequence 6, Appli
7	39	88.6	113	10	US-09-741-843-2 Sequence 2, Appli
8	39	88.6	113	10	US-09-741-843-6 Sequence 6, Appli
9	39	88.6	113	11	US-09-894-839-2 Sequence 2, Appli
10	39	88.6	113	11	US-09-894-839-6 Sequence 6, Appli
11	39	88.6	113	11	US-09-894-839-20 Sequence 20, Appl
12	39	88.6	113	11	US-09-988-013A-2 Sequence 2, Appli
13	39	88.6	113	11	US-09-988-013A-6 Sequence 6, Appli
14	35	79.5	272	12	US-10-053-530-14 Sequence 14, Appl
15	35	79.5	272	15	US-10-207-655-14 Sequence 14, Appl

16	33	75.0	902	15	US-10-231-778-222	Sequence 222, App
17	33	75.0	931	10	US-09-906-453-2	Sequence 2, Appli
18	32	72.7	235	9	US-09-815-242-5455	Sequence 5455, Ap
19	32	72.7	235	9	US-09-815-242-12684	Sequence 12684, A
20	32	72.7	272	11	US-09-774-639-167	Sequence 167, App
21	32	72.7	272	11	US-09-969-730-120	Sequence 120, App
22	31	70.5	368	15	US-10-205-823-377	Sequence 377, App
23	31	70.5	399	9	US-09-925-301-1385	Sequence 1385, Ap
24	31	70.5	588	10	US-09-908-193-34	Sequence 34, Appl
25	31	70.5	588	12	US-10-301-822-213	Sequence 213, App
26	31	70.5	695	9	US-09-764-898-191	Sequence 191, App
27	31	70.5	754	10	US-09-908-193-32	Sequence 32, Appl
28	31	70.5	776	10	US-09-908-193-33	Sequence 33, Appl
29	31	70.5	778	10	US-09-908-193-8	Sequence 8, Appli
30	31	70.5	779	10	US-09-908-193-10	Sequence 10, Appl
31	30	68.2	12	10	US-09-982-172-201	Sequence 201, App
32	30	68.2	12	10	US-09-982-172-249	Sequence 249, App
33	30	68.2	62	9	US-09-864-761-43345	Sequence 43345, A
34	30	68.2	162	10	US-09-923-246-2	Sequence 2, Appli
35	30	68.2	162	10	US-09-825-561A-10	Sequence 10, Appl
36	30	68.2	162	11	US-09-972-218A-19	Sequence 19, Appl
37	30	68.2	162	12	US-10-282-622-2	Sequence 2, Appli
38	30	68.2	162	12	US-10-282-622-6	Sequence 6, Appli
39	30	68.2	162	15	US-10-264-634-19	Sequence 19, Appl
40	30	68.2	162	15	US-10-295-723-2	Sequence 2, Appli
41	30	68.2	252	9	US-09-925-299-925	Sequence 925, App
42	30	68.2	252	11	US-09-925-299-925	Sequence 925, App
43	30	68.2	357	9	US-09-949-434-4	Sequence 4, Appli
44	30	68.2	483	10	US-09-881-752A-354	Sequence 354, App
45	30	68.2	519	10	US-09-923-246-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1

US-10-056-052-10
; Sequence 10, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-10

Query Match 100.0%; Score 44; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 95 HQYLSSYT 102

```
RESULT 2
US-10-056-052-14
; Sequence 14, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-14

Query Match      100.0%; Score 44; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HQYLSSYT 8
      |||||
Db      95 HQYLSSYT 102

RESULT 3
US-10-056-052-18
; Sequence 18, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-18

Query Match      100.0%; Score 44; DB 15; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HQYLSSYT 8
      |||||
Db      95 HQYLSSYT 102
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QY      1 HQYLSSYT 8
      |||||
Db      95 HQYLSSYT 102

RESULT 4
US-10-229-335-4
; Sequence 4, Application US/10229335
; Publication No. US20030144483A1
; GENERAL INFORMATION:
; APPLICANT: MEDAREX, INC.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
; IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; STREET: P.O. Box 953, 1545 Route 22 East
; CITY: Annandale
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/229,335
; FILING DATE: 26-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-229-335-4

Query Match      88.6%; Score 39; DB 12; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches      7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 HQYLSSYT 8
      |||||
Db      95 HQYLSSWT 102

RESULT 5
US-10-229-335-28
; Sequence 28, Application US/10229335
; Publication No. US20030144483A1
; GENERAL INFORMATION:
; APPLICANT: MEDAREX, INC.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
; IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; STREET: P.O. Box 953, 1545 Route 22 East
; CITY: Annandale
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08801
; COMPUTER READABLE FORM:
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;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: ASCII text
;/
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/10/229,335
;/ FILING DATE: 26-Aug-2002
;/ CLASSIFICATION: <Unknown>
;/
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/435,516
;/ FILING DATE: <Unknown>
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Arnold, Beth E.
;/ REGISTRATION NUMBER: 35,430
;/ REFERENCE/DOCKET NUMBER: MXI-013
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (617) 227-7400
;/ TELEFAX: (617) 227-5941
;/
;/ INFORMATION FOR SEQ ID NO: 28:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 112 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ FRAGMENT TYPE: internal
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-229-335-28

Query Match 88.6%; Score 39; DB 12; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

RESULT 6
US-10-056-052-6
; Sequence 6, Application US/10056052
; Publication No. US20030099656A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P0706US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-056-052-6

Query Match 88.6%; Score 39; DB 15; Length 112;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

Db 95 HQYLSSHT 102
RESULT 7
US-09-741-843-2
; Sequence 2, Application US/09741843
; Patent No. US20020102254A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
; TITLE OF INVENTION: AND LEUKEMIA CELLS
; FILE REFERENCE: 018733/0996
; CURRENT APPLICATION NUMBER: US/09/741,843
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-741-843-2

Query Match 88.6%; Score 39; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

RESULT 8
US-09-741-843-6
; Sequence 6, Application US/09741843
; Patent No. US20020102254A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
; TITLE OF INVENTION: AND LEUKEMIA CELLS
; FILE REFERENCE: 018733/0996
; CURRENT APPLICATION NUMBER: US/09/741,843
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-741-843-6

Query Match 88.6%; Score 39; DB 10; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
Db 95 HQYLSSWT 102

RESULT 9
US-09-894-839-2
; Sequence 2, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-894-839-2

Query Match 88.6%; Score 39; DB 11; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
|||||:
Db 95 HQYLSSWT 102

RESULT 10
US-09-894-839-6
; Sequence 6, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-839-6

Query Match 88.6%; Score 39; DB 11; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
|||||:
Db 95 HQYLSSWT 102

RESULT 11
US-09-894-839-20
; Sequence 20, Application US/09894839
; Publication No. US20030035800A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans

; APPLICANT: QU, Zhengxing
; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
; FILE REFERENCE: 018733/1049
; CURRENT APPLICATION NUMBER: US/09/894,839
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/155,107
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/013,709
; PRIOR FILING DATE: 1996-03-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-839-20

Query Match 88.6%; Score 39; DB 11; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
|||||:
Db 95 HQYLSSWT 102

RESULT 12
US-09-988-013A-2
; Sequence 2, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; FILE REFERENCE: 18733/1082
; CURRENT APPLICATION NUMBER: US/09/988,013A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-988-013A-2

Query Match 88.6%; Score 39; DB 11; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
|||||:
Db 95 HQYLSSWT 102

RESULT 13
US-09-988-013A-6
; Sequence 6, Application US/09988013A
; Publication No. US20030103979A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, Shui-on
; APPLICANT: HANSEN, Hans
; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-
; FILE REFERENCE: 18733/1082

; CURRENT APPLICATION NUMBER: US/09/988,013A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/741,843
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/127,902
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/690,102
; PRIOR FILING DATE: 1996-07-06
; PRIOR APPLICATION NUMBER: US 08/289,576
; PRIOR FILING DATE: 1994-08-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-988-013A-6

Query Match 88.6%; Score 39; DB 11; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||||:|
Db 95 HQYLSSWT 102

RESULT 14

US-10-053-530-14
; Sequence 14, Application US/10053530
; Publication No. US20030133939A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey
; APPLICANT: Hayden-Ledbetter, Martha
; TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 390069.401
; CURRENT APPLICATION NUMBER: US/10/053,530
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 09/765,208
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
LOCATION: (1)..(272)
OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-10-053-530-14

Query Match 79.5%; Score 35; DB 12; Length 272;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||||:|
Db 115 HQFLSSWT 122

RESULT 15

US-10-207-655-14
; Sequence 14, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
LOCATION: (1)..(272)
OTHER INFORMATION: MOUSE ANTI-HUMAN CD22 SCFV
US-10-207-655-14

Query Match 79.5%; Score 35; DB 15; Length 272;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||||:|
Db 115 HQFLSSWT 122

Search completed: August 13, 2003, 09:43:43
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw_model

Run on: August 13, 2003, 09:43:16 ; Search time 38 Seconds
(without alignments)
20.246 Million cell updates/sec

Title: US-10-056-052A-29
Perfect score: 44
Sequence: 1 HQYLSSYT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	103	2 PH1054	Ig light chain V r
2	37	84.1	101	2 S26337	Ig light chain V r
3	34	77.3	88	2 C82627	hypothetical prote
4	34	77.3	468	2 E81924	probable two-compo
5	34	77.3	543	2 A32693	steroid receptor p
6	34	77.3	746	2 B32693	steroid receptor p
7	34	77.3	1226	2 H64479	protoporphylin IX
8	34	77.3	1481	2 S78373	DNA-directed RNA p
9	34	77.3	2531	2 T31070	notch homolog - se
10	33	75.0	113	2 S66936	probable membrane
11	33	75.0	462	2 C81701	hypothetical prote
12	33	75.0	554	2 A56596	chitinase (EC 3.2.
13	33	75.0	730	2 T16455	hypothetical prote
14	33	75.0	796	2 AG1849	serine/threonine k
15	33	75.0	902	2 T01127	curly leaf protein
16	32	72.7	215	1 SXADMS	hexon-associated p
17	32	72.7	226	2 D90054	glucuronate operon t
18	32	72.7	245	2 D71554	probable adenylate
19	32	72.7	294	2 AF1218	Salmonella typhimu
20	32	72.7	294	2 AII571	Regulatory protein
21	32	72.7	586	2 JC6500	hnf-3/forkhead tra
22	32	72.7	610	2 C96732	hypothetical prote
23	32	72.7	663	2 T40493	hnf-3/forkhead tra
24	32	72.7	1086	2 T40354	hypothetical prote
25	32	72.7	1628	2 T38055	hypothetical prote
26	31	70.5	138	2 T21299	hypothetical prote
27	31	70.5	149	2 D84181	hypothetical prote
28	31	70.5	218	2 D64227	major sigma factor
29	31	70.5	234	2 T24374	hypothetical prote

30	31	70.5	297	2 D83825	hypothetical prote
31	31	70.5	341	2 T16951	hypothetical prote
32	31	70.5	368	2 S54160	spermine synthase
33	31	70.5	410	2 S28485	lipopolysaccharide
34	31	70.5	506	2 T07209	H+-transporting tw
35	31	70.5	553	2 T40438	hypothetical prote
36	31	70.5	588	2 A49618	probable ataxia-te
37	31	70.5	620	2 E82351	ATP-dependent DNA
38	31	70.5	776	2 S28258	androgen-regulated
39	31	70.5	1148	2 T18770	probable calcium c
40	31	70.5	1279	2 T17194	protoporphylin IX
41	31	70.5	4436	2 E71086	hypothetical prote
42	30	68.2	103	2 G42528	B26R protein - vac
43	30	68.2	111	2 G30502	Ig kappa chain V r
44	30	68.2	161	2 E84201	hypothetical prote
45	30	68.2	204	2 T25709	hypothetical prote

ALIGNMENTS

RESULT 1
PH1054
Ig light chain V region (clone 202.135) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1054
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1054
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-103 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 44; DB 2; Length-103;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HQYLSSYT 8
|||
Db 95 HQYLSSYT 102

RESULT 2
S26337
Ig light chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C:Accession: S26337; S78449
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26337
A:Molecule type: mRNA
A:Residues: 1-101 <STA>
A:Cross-references: EMBL:X59193
R:Caton, A.J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S78447
A:Accession: S78449
A:Molecule type: mRNA
A:Residues: 1-60, 'T', '62-91, 'S', '93-101 <CAT>
A:Cross-references: EMBL:X59193; NID:g52323; PIDN:CAA41903.1; PID:g1334067
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-88/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 37; DB 2; Length 101;
Best Local Similarity 75.0%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
| | | | | | | |
Db 87 HQYLSTFT 94

RESULT 3
C82627
hypothetical protein XF1883 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: C82627
R;anonymouse, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
Note: for a complete list of authors see reference number A59328 below
A;Accession: C82627
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <SIM>
A;Cross-references: GB:AE004008; GB:AE003849; NID:g9106961; PIDN:AAF84689.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1883

Query Match 77.3%; Score 34; DB 2; Length 88;
Best Local Similarity 75.0%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 HQYLSSYT 8
| | | | | | | |
Db 15 HQYISLT 22

RESULT 4
E81924
probable two-component system sensor kinase (EC 2.7.3.-) NMA0797 [imported] - Neisseria
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: E81924
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: E81924
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-468 <PAR>
A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84080.1; PID:g737951
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA0797
C;Keywords: Phosphotransferase

Query Match 77.3%; Score 34; DB 2; Length 468;
Best Local Similarity 62.5%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
| | | | | | | |
Db 93 HRYDSYT 100

RESULT 5
A32693
steroid receptor protein svp 1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
C;Accession: A32693
R;Mlodzik, M.; Hiromi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.
Cell 60, 211-224, 1990
A;Title: The Drosophila seven-up gene, a member of the steroid receptor gene superfam
A;Reference number: A32693; MUID:90124631; PMID:2105166
A;Accession: A32693
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-543 <MLO>
A;Cross-references: GB:M28863; NID:g158518; PIDN:AAA62770.1; PID:g158519
C;Genetics:
A;Gene: FlyBase:svp
A;Cross-references: FlyBase:FBgn0003651
C;Superfamily: unassigned erba-related proteins; erba transforming protein homology
C;Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcriptio
F;198-452/Domain: erba transforming protein homology <ERBA>
F;200-220/Region: zinc finger
F;236-260/Region: zinc finger

Query Match 77.3%; Score 34; DB 2; Length 543;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
| | | | | | |
Db 305 HSYLSSY 311

RESULT 6
B32693
steroid receptor protein svp 2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 12-Sep-1997
C;Accession: B32693
R;Mlodzik, M.; Hiromi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.
Cell 60, 211-224, 1990
A;Title: The Drosophila seven-up gene, a member of the steroid receptor gene superfam
A;Reference number: A32693; MUID:90124631; PMID:2105166
A;Accession: B32693
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-746 <MLO>
A;Cross-references: GB:M28863; GB:M28864
C;Genetics:
A;Gene: FlyBase:svp
A;Cross-references: FlyBase:FBgn0003651
C;Superfamily: unassigned erba-related proteins; erba transforming protein homology
C;Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcriptio
F;198-452/Domain: erba transforming protein homology <ERBA>
F;200-220/Region: zinc finger
F;236-260/Region: zinc finger

Query Match 77.3%; Score 34; DB 2; Length 746;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
| | | | | | |

Db 305 HSYLSSY 311

RESULT 7
H64479
protoporphyrin IX magnesium chelatase (EC 4.99.1.-) homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
C:Accession: H64479
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: H64479
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
Residues: 1-1226 <BUL>
Cross-references: GB:U67585; GB:L77117; NID:gl592088; PIDN:AAB99452.1; PID:gl500323; T
Genetics:
A:Map position: FOR1408283-1411963
C:Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
C:Keywords: lyase

Query Match 77.3%; Score 34; DB 2; Length 1226;
Best Local Similarity 71.4%; Pred. No. 92;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
|||:|
Db 509 HQVIASY 515

RESULT 8
S78373
DNA-directed RNA polymerase (EC 2.7.7.6) beta'' chain - Odontella sinensis chloroplast
C:Species: chloroplast Odontella sinensis
C:Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 20-Jun-2000
C:Accession: S78373
R:Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A:Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sinensis
A:Reference number: S78238
A:Accession: S78373
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
Residues: 1-1481 <KOW>
Cross-references: EMBL:Z67753; NID:gl185127; PID:gl185263
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C:Genetics:
A:Gene: rpoC2
A:Genome: chloroplast
C:Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain
C:Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 77.3%; Score 34; DB 2; Length 1481;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||:|
Db 924 HQFIDSYT 931.

RESULT 9
T31070
notch homolog - sea urchin (Lytechinus variegatus)
C:Species: Lytechinus variegatus (variegated urchin)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C:Accession: T31070
R:Sherwood, D.R.; McClay, D.R.

Development 124, 3363-3374, 1997
A:Title: Identification and localization of a sea urchin Notch homologue: insights in
A:Reference number: Z20966; MUID:97454256; PMID:9310331
A:Accession: T31070
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-2531 <SHE>
A:Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 77.3%; Score 34; DB 2; Length 2531;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|||:|
Db 949 HEYVDSYT 956

RESULT 10
S66936
probable membrane protein YOR053w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O2799
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C:Accession: S66936; S66927
R:Bohn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D.V.; Valens, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66929
A:Accession: S66936
A:Molecule type: DNA
A:Residues: 1-113 <BOH>
A:Cross-references: EMBL:Z74961; NID:gl420188; PID:e252336; PID:gl420189; MIPS:YOR053
A:Experimental source: strain S288C
R:Landt, O.; Hiesel, R.; Unseld, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66907
A:Accession: S66927
A:Molecule type: DNA
A:Residues: 1-8 <LAN>
A:Cross-references: EMBL:Z74961; MIPS:YOR053w
A:Experimental source: strain S288C
C:Genetics:
A:Cross-references: SGD:S0005579
A:Map position: 15R
C:Keywords: transmembrane protein
F:3-19/Domain: transmembrane #status predicted <TMM>

Query Match 75.0%; Score 33; DB 2; Length 113;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
|||:|
Db 82 HQYRSSY 88

RESULT 11
C81701
hypothetical protein TC0441 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MOPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C:Accession: C81701
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MOPn and Chlamydia pneumoniae AR39
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: C81701
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-462 <TET>
A:Cross-references: GB:AE002313; GB:AE002160; NID:g7190484; PIDN:AAF39295.1; PID:g719

A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0441

Query Match 75.0%; Score 33; DB 2; Length 462;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
|:|:|:|
Db 440 HEYLSTY 446

RESULT 12
A56596
Chitinase (EC 3.2.1.14) - tobacco hornworm
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 29-Jan-1999
C;Accession: A56596

Kramer, K.J.; Corpuz, L.; Choi, H.K.; Muthukrishnan, S.
sect Biochem. Mol. Biol. 23, 691-701, 1993
Title: Sequence of a cDNA and expression of the gene encoding epidermal and gut chitinase from the tobacco hornworm, Manduca sexta.
A;Reference number: A56596; MUID:93357793; PMID:8353525

A;Accession: A56596
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-554 <KRA>
A;Cross-references: GB:U02270; GB:S64757; NID:g406048; PID:g406049

A;Experimental source: larvae
A;Note: sequence extracted from NCBI backbone (NCBIN:136417, NCBIP:136418)
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 75.0%; Score 33; DB 2; Length 554;
Best Local Similarity 62.5%; Pred. No. 64;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|:|:|:|
Db 392 HKHMSSYT 399

RESULT 13
T16455
hypothetical protein F55D10.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16455
B;Leimbach, D.
Submitted to the EMBL Data Library, November 1995
Description: The sequence of C. elegans cosmid F55D10.
A;Reference number: Z18516

A;Accession: T16455
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-730 <LEI>
A;Cross-references: EMBL:U40948; NID:gl072223; PID:gl072224; PIDN:AAA81727.1; CESP:F55D10.3
C;Genetics:
A;Gene: CESP:F55D10.3
A;Introns: 48/3; 125/3; 181/3

Query Match 75.0%; Score 33; DB 2; Length 730;
Best Local Similarity 62.5%; Pred. No. 86;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|:|:|:|
Db 430 HEYLKSYS 437

RESULT 14
AG1849
serine/threonine kinase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG1849
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriqui
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG1849
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-796 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAW72302.1; PID:gl17129689; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr0344

Query Match 75.0%; Score 33; DB 2; Length 796;
Best Local Similarity 71.4%; Pred. No. 94;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
|:|:|:|
Db 147 HQYVTSY 153

RESULT 15
T01127
curly leaf protein (polycarb-group) [imported] - Arabidopsis thaliana
N;Alternate names: curly leaf protein homolog F26B6.3
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 02-Feb-2001
C;Accession: T01127; A84624
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke
submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.
A;Reference number: Z14198

A;Accession: T01127
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-902 <ROU>
A;Cross-references: EMBL:AC003040; NID:g3242700; PID:g3242729
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84624
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-902 <STO>
A;Cross-references: GB:AE002093; NID:g3242729; PIDN:AAC23781.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g23380; F26B6.3
A;Map position: 2
A;Introns: 21/3; 52/3; 153/2; 207/2; 235/3; 280/3; 296/3; 320/3; 554/2; 604/3; 679/2;

Query Match 75.0%; Score 33; DB 2; Length 902;
Best Local Similarity 62.5%; Pred. No. 11e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|:|:|:|
Db 775 HEYLGEYT 782

Search completed: August 13, 2003, 09:48:14
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: August 13, 2003, 09:40:00 ; Search time 23. Seconds
(without alignments)
16.357 Million cell updates/sec

Title: US-10-056-052A-29
Perfect score: 44
Sequence: 1 HQYLSSYT 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	77.3	543	1 7UPL_DROME	P16375 drosophila
2	34	77.3	746	1 7UP2_DROME	P16376 drosophila
3	34	77.3	1481	1 RPOD_ODOSI	P49468 odontella s
4	33	75.0	554	1 CHIT_MANSE	P36362 manduca sex
5	33	75.0	902	1 CLF_ARATH	P93831 arabidopsis
6	32	72.7	215	1 HEX8_ADEM1	P19722 mouse adeno
7	32	72.7	245	1 KAD_CHLTR	O84130 chlamydia t
8	32	72.7	663	1 SEPI_SCHPO	O43058 schizosacch
9	32	72.7	1628	1 YATE_SCHPO	O09779 schizosacch
10	31	70.5	218	1 Y248_MYCGE	P47490 mycoplasma
11	31	70.5	341	1 YSX3_CAEEL	Q10022 caenorhabdi
12	31	70.5	366	1 SPSY_HUMAN	P52788 homo sapien
13	31	70.5	366	1 SPSY_MOUSE	P97355 mus musculu
14	31	70.5	391	1 CGA1_CARAU	Q92161 carassius a
15	31	70.5	506	1 ATPA_CHLVU	P56294 chlorella v
16	31	70.5	553	1 ME18_SCHPO	Q9uub3 schizosacch
17	31	70.5	754	1 AD07_HUMAN	Q9h2u9 homo sapien
18	31	70.5	776	1 AD07_MACFA	Q28475 macaca fasc
19	31	70.5	1279	1 BCHH_CHLVI	O50314 chlorobium
20	30	68.2	103	1 VC20_VACCC	P21104 vaccinia vi
21	30	68.2	359	1 MANR_PSEPU	P11444 pseudomonas
22	30	68.2	377	1 PMK1_CAEEL	Q17446 caenorhabdi
23	30	68.2	410	1 COT2_CHICK	Q90733 gallus gall
24	30	68.2	414	1 COT2_BOVIN	Q9ttt7 bos taurus
25	30	68.2	414	1 COT2_HUMAN	P24468 homo sapien
26	30	68.2	414	1 COT2_MOUSE	P43135 mus musculu
27	30	68.2	414	1 COT2_RAT	O09018 rattus norv
28	30	68.2	444	1 EX7L_RICCN	Q92gu6 rickettsia
29	30	68.2	655	1 ABG2_HUMAN	Q9unq0 homo sapien
30	30	68.2	766	1 PRTP_HSVEB	P28973 equine herp
31	30	68.2	910	1 HUL5_YEAST	P53119 saccharomyc
32	30	68.2	925	1 NPPI_HUMAN	P22413 h ectonucle
33	30	68.2	1050	1 BUIB_HUMAN	O60566 homo sapien

ALIGNMENTS

RESULT 1

ID	7UPL_DROME	STANDARD;	PRT;	543 AA.
AC	P16375; Q9VGB0;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Steroid receptor seven-up type 1.			
GN	SVP OR NR2F3 OR CG11502.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90124631; PubMed=2105166;			
RA	Mlodzik M., Hiromi Y., Weber U., Goodman C.S., Rubin G.M.;			
RT	"The Drosophila seven-up gene, a member of the steroid receptor gene			
RT	superfamily, controls photoreceptor cell fates."			
RL	Cell 60:211-224(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Berkeley;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blaize R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,			
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,			
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,			
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,			

34	30	68.2	1729	1	RRP5_YEAST	Q05022	saccharomyc
35	30	68.2	2703	1	NOTC_DROME	P07207	drosophila
36	29	65.9	104	1	Y079_NPVOP	O10332	orgyia pseu
37	29	65.9	157	1	ATPX_GALSU	P35012	galdieria s
38	29	65.9	230	1	YD83_YEAST	Q04004	saccharomyc
39	29	65.9	264	1	Y061_UREPA	Q9pr84	ureaplasma
40	29	65.9	285	1	TESB_ECOLI	P23911	escherichia
41	29	65.9	310	1	ADPR_LACLA	Q06715	lactococcus
42	29	65.9	326	1	SCRR_PEDPE	P43472	pediococcus
43	29	65.9	390	1	SOX_MOUSE	Q9d826	mus musculu
44	29	65.9	391	1	ACKA_BACHD	Q9k815	bacillus ha
45	29	65.9	395	1	ACKA_BACSU	P37877	bacillus su

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
CC -!- FUNCTION: PUTATIVE RECEPTOR THAT IS REQUIRED IN PHOTORECEPTOR
CC CELLS PRECURSORS DURING EYE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name-Type 1;
CC IsoId=P16375-1; Sequence=Displayed;
CC Name-Type 2;
CC IsoId=P16376-1; Sequence=External;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF NEURAL PRECURSORS.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
CC subfamily.
CC -----
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CC -----
DR EMBL; M28863; AAA62770.1; -.
DR EMBL; AE003695; AAF54773.1; -.
DR PIR; A32693; A32693.
DR HSSP; P19793; 2NLL.
DR TRANSFAC; T02741; -.
DR FlyBase; FBgn0003651; svp.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0007510; P:cardioblast cell fate determination; IEP.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Stdhrmn_receptor.
DR InterPro; IPR001628; znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Vision; Alternative splicing.
FT DNA_BIND 200 265 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 200 220 C4-TYPE.
FT ZN_FING 236 260 C4-TYPE.
SQ SEQUENCE 543 AA; 57987 MW; 0BC189DCF1A27213 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 543;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
| | | | |
Db 305 HSYLSSY 311

RESULT 2
7UP2_DROME
ID 7UP2_DROME STANDARD; PRT; 746 AA.
AC P16376;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Steroid receptor seven-up type 2.
GN SVP OR NR2F3.
OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90124631; PubMed=2105166;
RA Mlodzik M., Hiromi Y., Weber U., Goodman C.S., Rubin G.M.;
RT "The Drosophila seven-up gene, a member of the steroid receptor gene
RT superfamily, controls photoreceptor cell fates.";
RL Cell 60:211-224(1990).
CC -!- FUNCTION: PUTATIVE RECEPTOR THAT IS REQUIRED IN PHOTORECEPTOR
CC CELLS PRECURSORS DURING EYE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name-Type 2;
CC IsoId=P16376-1; Sequence=Displayed;
CC Name-Type 1;
CC IsoId=P16375-1; Sequence=External;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF NEURAL PRECURSORS.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
CC subfamily.
CC -----
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CC -----
DR EMBL; M28864; AAA03014.1; -.
DR PIR; B32693; B32693.
DR HSSP; P19793; 2NLL.
DR FlyBase; FBgn0003651; svp.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Stdhrmn_receptor.
DR InterPro; IPR001628; znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Vision; Alternative splicing.
FT DNA_BIND 200 265 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 200 220 C4-TYPE.
FT ZN_FING 236 260 C4-TYPE.
SQ SEQUENCE 746 AA; 76830 MW; 7F256AFD4165326D CRC64;

Query Match 77.3%; Score 34; DB 1; Length 746;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
| | | | |
Db 305 HSYLSSY 311

RESULT 3
RPOD_ODOSI
ID RPOD_ODOSI STANDARD; PRT; 1481 AA.
AC P49468;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
GN RPOC2.
OS Odontella sinensis (Marine centric diatom).

OG Chloroplast.
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
OC Biddulphiophycidae; Eupodiscales; Eupodisaceae; Odontella.
OX NCBI_TaxID=2839;
RN [1]
RP SEQUENCE FROM N.A.
RA Kowalik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.;
RT "The chloroplast genome of a chlorophyll a+c-containing alga,
RT Odontella sinensis";
RL Plant Mol. Biol. Rep. 13:336-342(1995).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -!- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four
CC subunits: alpha, beta, beta', and beta".
CC -----
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CC -----
CC EMBL; Z67753; CAA91746.1; -.
DR PIR; S78373; S78373.
DR HSSP; Q9KWU6; 1HQM.
DR InterPro; IPR000722; RNA_pol_A.
DR InterPro; IPR007066; RNA_pol_Rpb1_3.
DR InterPro; IPR007083; RNA_pol_Rpb1_4.
DR InterPro; IPR007081; RNA_pol_Rpb1_5.
DR Pfam; PF04983; RNA_pol_Rpb1_3; 1.
DR Pfam; PF05000; RNA_pol_Rpb1_4; 1.
DR Pfam; PF04998; RNA_pol_Rpb1_5; 2.
DR Transferrase; Transcription; DNA-directed RNA polymerase; Chloroplast.
KW SEQUENCE 1481 AA; 170974 MW; 184936FB2A577228 CRC64;
SQ

Query Match 77.3%; Score 34; DB 1; Length 1481;
Best Local Similarity 62.5%; Pred. No. 75;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
Db 924 HQFIDSYT 931

RESULT 4
CLF_ARATH
ID CHIT_MANSE STANDARD; PRT; 554 AA.
AC P36362;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Endochitinase precursor (EC 3.2.1.14).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93357793; PubMed=8353525;
RA Kramer K.J., Corpuz L., Choi H.K., Muthukrishnan S.;
RT "Sequence of a cDNA and expression of the gene encoding epidermal and
RT gut chitinases of Manduca sexta";
RL Insect Biochem. Mol. Biol. 23:691-701(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97215580; PubMed=9061927;
RA Choi H.K., Choi K.H., Kramer K.J., Muthukrishnan S.;
RT "Isolation and characterization of a genomic clone for the gene of an

RT Insect molting enzyme, chitinase.";
RL Insect Biochem. Mol. Biol. 27:37-47(1997).
CC -!- FUNCTION: DIGEST CHITIN IN THE EXOSKELETON DURING THE MOLTING
CC PROCESS.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC acetyl-D-glucosamine polymers of chitin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: EPIDERMIS AND GUT.
CC -!- DEVELOPMENTAL STAGE: HIGH LEVELS SEEN IN THE EPIDERMIS ON DAY 0,
CC BUT RAPIDLY DISAPPEARS AND IS UNDETECTED ON DAYS 1-4 OF FIFTH
CC INSTAR. IT REAPPEARS ON DAY 5 AND PEAKS ON DAY 7 AFTER WHICH A
CC RAPID DECLINE IS SEEN. IN THE GUT IS DETECTED ON DAY 6 WITH LOWER
CC LEVELS SEEN ON DAYS 0, 7 AND 8.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
CC HYDROLASES).
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CC -----
CC EMBL; U02270; AAC04924.1; -.
DR EMBL; L49234; AAB53952.1; -.
DR PIR; A56596; A56596.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18/2.
DR Pfam; PF01607; CBM_14; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00494; ChtBD2; 1.
DR SMART; SM00636; Glyco_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Signal; Glycoprotein.
FT SIGNAL 1 19
FT CHAIN 20 554
FT DOMAIN 396 453
FT ACT_SITE 146 146
FT CARBOHYD 85 85
FT CARBOHYD 303 303
FT CARBOHYD 407 407
FT CARBOHYD 545 545
SQ SEQUENCE 554 AA; 62203 MW; 3989D756C96CD490 CRC64;

Query Match 75.0%; Score 33; DB 1; Length 554;
Best Local Similarity 62.5%; Pred. No. 42;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
Db 392 HKHMSSYT 399

RESULT 5
CLF_ARATH
ID CLF_ARATH STANDARD; PRT; 902 AA.
AC P93831; O80455;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Polycomb group protein CURLY LEAF.
GN CLF OR AT2G23380 OR F26B6.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC STRAIN=cv. Landsberg erecta; TISSUE=Flower;

RX MEDLINE=97205275; PubMed=9052779;
RA Goodrich J., Puangsomlee P., Martin M., Long D., Meyerowitz E.M.,
RA Coupland G.;
RT "A Polycomb-group gene regulates homeotic gene expression in
RT Arabidopsis.";
RL Nature 386:44-51(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buehl C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
BT Nature 402:761-768(1999).
CC -!- FUNCTION: Polycomb group (PcG) protein. Required to regulate
CC floral development by repressing the AGAMOUS homeotic gene in
CC leaves, inflorescence stems and flowers. PcG proteins act by
CC forming multiprotein complexes, which are required to maintain the
CC transcriptionally repressive state of homeotic genes throughout
CC development. PcG proteins are not required to initiate repression,
CC but to maintain it during later stages of development. They
CC probably act via the methylation of histones, rendering chromatin
CC heritably changed in its expressibility. May constitute the
CC catalytic subunit of a potential methyltransferase activity of PcG
CC complexes.
CC -!- SUBUNIT: Probable component of a PcG complex. In plants, PcG
CC complexes are probably composed of a member of the EZ family (CLF
CC or MEA), FIE, and a member of the VEFs family (FIS2, VRN2 or
CC EMF2) (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- TISSUE SPECIFICITY: Strongly expressed throughout the apical
CC meristem, leaf primordia, and leaves of 7-8 day-old seedling.
CC Weakly expressed in the vasculature of hypocotyl. Strongly
CC expressed throughout the young stages 1 and 2 floral meristems
CC that arose on the flanks of the apex. In stage 3 and 4 flowers, it
CC is expressed in the emerging sepal primordia and in the dome of
CC the floral meristem. During stages 6 and 7, it is strongly
CC expressed in developing petal and stamen, and weakly expressed in
CC the sepals. Late in floral development, at stage 12, it is weakly
CC expressed in all floral whorls, and expressed at intermediate
CC level in petals and ovules.
CC -!- DEVELOPMENTAL STAGE: Expressed in all four whorls throughout
CC flower development.
CC -!- SIMILARITY: BELONGS TO THE EZ FAMILY.
CC -!- SIMILARITY: Contains 1 SANT domain.
CC -!- SIMILARITY: Contains 1 SET domain.
CC -----
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CC -----
CC EMBL; Y10580; CAA71599.1; -
CC EMBL; AC003040; AAC23781.1; -
CC InterPro; IPR001005; Myb_DNA_binding.
CC InterPro; IPR001214; SET.
CC Pfam; PF00856; SET; 1.
CC SMART; SM00717; SANT; 1.
CC SMART; SM00317; SET; 1.
CC PROSITE; PS50280; SET; 1.
KW Transcription regulation; Repressor; Flowering; Nuclear protein;
KW Developmental protein.
FT DOMAIN 531 581 SANT.

FT DOMAIN 649 720 CYS-RICH.
FT DOMAIN 751 871 SET.
FT CONFLICT 225 225 S -> N (IN REF. 2).
FT CONFLICT 332 332 T -> P (IN REF. 2).
FT CONFLICT 415 415 K -> N (IN REF. 2).
FT CONFLICT 658 658 K -> Q (IN REF. 2).
FT CONFLICT 674 674 C -> Y (IN REF. 2).
FT CONFLICT 761 761 V -> I (IN REF. 2).
SQ SEQUENCE 902 AA; 100369 MW; 90B45ED27D219D64 CRC64;

Query Match 75.0%; Score 33; DB 1; Length 902;
Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
Db 775 HEYLGEYT 782

RESULT 6
HEX8_ADEMI
ID HEX8_ADEMI STANDARD; PRT; 215 AA.
AC P19722;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hexon-associated protein precursor (Protein VIII).
GN PVIII.
OS Mouse adenovirus type 1 (MAV-1).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90064816; PubMed=2531236;
RA Raviprakash K.S., Grunhaus A., el Kholy M.A., Horwitz M.S.;
RT "The mouse adenovirus type 1 contains an unusual E3 region.";
RL J. Virol. 63:5455-5458(1989).
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CC -----
CC EMBL; M30594; AAA42432.1; -
CC PIR; A33382; SXADMS.
CC InterPro; IPR000646; Adeno_PVIII.
CC Pfam; PF01310; Adeno_PVIII; 1.
KW Hexon-associated protein.
FT PROPEP 1 109 POTENTIAL.
FT CHAIN 110 215 HEXON-ASSOCIATED PROTEIN.
FT SITE 109 110 CLEAVAGE (BY ADENOVIRUS PROTEASE)
FT SEQUENCE 215 AA; 23272 MW; 739F0BE85408D7A1 CRC64;

Query Match 72.7%; Score 32; DB 1; Length 215;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
Db 198 HQFLSNY 204

RESULT 7
KAD_CHLTR
ID KAD_CHLTR STANDARD; PRT; 245 AA.
AC O84130;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK OR CT128.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammell C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RT Science 282:754-759(1998).
RL -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the adenylate kinase family.

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CC EMBL: AE001286; AAC67719.1; -.
DR PIR: D71554; D71554.
DR HSSP: P08760; 2AK3.
DR HAMAP: MF_00235; -; 1.
DR InterPro; IPR006259; Adenyl_kin_sub.
DR InterPro; IPR000850; Adenylate_kin.
DR Pfam: PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYITKNASE.
DR ProDom; PD000657; Adenylate_kin; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW Transferase; Kinase; ATP-binding; Complete proteome.
FT NP_BIND 12 20 ATP (BY SIMILARITY).
SQ SEQUENCE 245 AA; 27784 MW; 3F38D306ED75D09F CRC64;

Query Match 72.7%; Score 32; DB 1; Length 245;
Best Local Similarity 71.4%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 HQYLSSY 7
115 HEFLSSY 121
|::|

RESULT 8
SEPI_SCHPO STANDARD; PRT; 663 AA.
ID SEPI_SCHPO STANDARD; PRT; 663 AA.
AC O43058; P79006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Forkhead protein sepl.
GN SEPI OR SPBC4C3.12.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98087410; PubMed=9427538;
RA Ribar B., Banrevi A., Sipiczki M.;
RT "sepl+ encodes a transcription-factor homologue of the HNF-3/forkhead

RT DNA-binding-domain family in Schizosaccharomyces pombe.";
RL Gene 202:1-5(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Contains 1 fork-head domain.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 86
CC TO 123, FROM POSITION 583 ONWARD AND IS SHORTER (586 AA) DUE TO
CC FRAMESHIFTS.

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CC EMBL: U88191; AAC49903.1; ALT_FRAME.
DR EMBL: AL021730; CAA16826.1; -.
DR PIR: T40493; T40493.
DR HSSP: Q63245; 2HFH.
DR GeneDB_SPombe; SPBC4C3.12; -.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; FALSE_NEG.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS50039; FORK_HEAD_3; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
FT DNA_BIND 128 222 PVSHLEKDVET -> TCITFGECCN (IN REF. 1).
FT CONFLICT 377 387
SQ SEQUENCE 663 AA; 73031 MW; A66099437B7714C2 CRC64;

Query Match 72.7%; Score 32; DB 1; Length 663;
Best Local Similarity 71.4%; Pred. No. 81;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
|::|
Db 262 HQYLQNY 268

RESULT 9
YATE_SCHPO STANDARD; PRT; 1628 AA.
AC Q09779; 013884;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C1D4.14 in chromosome I.
GN SPAC1D4.14 OR SPAC22F3.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=2184801; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Wolckart G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -!- SIMILARITY: TO YEAST RLR1.

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CC EMBL; 269239; CAA93223.1; -.
DR EMBL; 254285; CAA91079.2; -.
DR PIR; T38055; T38055.
DR GeneDB_SPombe; SPAC1D4.14; -.
KW Hypothetical protein.
SQ SEQUENCE 1628 AA; 188831 MW; 85A30FB43D2CAED0 CRC64;

Query Match 72.7%; Score 32; DB 1; Length 1628;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HOYLSSY 7
|:|:|:
Db 1209 HKYLTYS 1215

RESULT 10
Y248_MYCGE
ID Y248_MYCGE STANDARD; PRT; 218 AA.

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P47490;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG248.
GN MG248.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bost K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).

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CC EMBL; U39703; AAC71468.1; -.
DR PIR; D64227; D64227.
DR TIGR; MG248; -.
DR InterPro; IPR006901; DUF633.
DR Pfam; PF04816; DUF633; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 218 AA; 25187 MW; E213395E1B87CB7D CRC64;

Query Match 70.5%; Score 31; DB 1; Length 218;
Best Local Similarity 71.4%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HOYLSSY 7
|:|:|:
Db 27 HSYLTYS 33

RESULT 11
YSX3_CAEEL STANDARD; PRT; 341 AA.
ID YSX3_CAEEL
AC Q10022;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 39.0 kDa protein T28D9.3 in chromosome II.
GN T28D9.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: WEAK, TO YEAST D9719.9.

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CC -----
DR EMBL; U28738; AAA68312.1; -
DR PIR; T16951; T16951.
DR WormPep; T28D9.3; CE02068.
DR InterPro; IPR000326; PA_PTPase.
DR Pfam; PF01569; PAP2; 1.
DR SMART; SM00014; acidPPc; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 71 91 POTENTIAL.
FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 223 243 POTENTIAL.
FT TRANSMEM 257 277 POTENTIAL.
SQ SEQUENCE 341 AA; 39028 MW; DF74E39BC3E2DA8E CRC64;

Query Match 70.5%; Score 31; DB 1; Length 341;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 171 HRYITDYT 178
1 HQYLSSYT 8
|:|:|

RESULT 12
SPSY_HUMAN STANDARD; PRT; 366 AA.
AC P52788; O00544;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Spermine synthase (EC 2.5.1.22) (Spermidine aminopropyltransferase) (SPMSY).
GN SMS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96027753; PubMed=7546290;
RA Koronen V.-P., Halmekytoe M., Kauppinen L., Myoehaenen S., Wahlfors J., Keinonen T., Hyvoenen T., Alhonen L., Eloranta T., Jaenne J.;
RT "Molecular cloning of a cDNA encoding human spermine synthase."; DNA Cell Biol. 14:841-847(1995).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=97446142; PubMed=9299240;
RA Grief M., Whyte M.P., Thakker R.V., Mazzarella R.;
RT "Sequence analysis of 139 kb in Xp22.1 containing spermine synthase and the 5' region of PEX."; Genomics 44:227-231(1997).
RN [3]
SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP PARTIAL SEQUENCE.
RA Eloranta T., Kajander O., Kauppinen L., Hyvoenen T., Linnala-Kankkunen A., Kalkkinen N., Kulomaa M., Alhonen L., Jaenne J.;
RL (In) Goldemberg S.H., Algranati I.D. (eds.); Proceedings of the international symposium on the biology and chemistry of polyamines, pp.91-98, ICSU Press, New York (1988).
RL -!- CATALYTIC ACTIVITY: S-adenosylmethioninamine + spermidine = 5'-methylthioadenosine + spermine.
CC -!- PATHWAY: BIOSYNTHESIS OF SPERMINE FROM SPERMIDINE.
CC -!- SIMILARITY: BELONGS TO THE SPERMIDINE/SPERMINE SYNTHASES FAMILY.
CC -----
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CC -----
DR EMBL; Z49099; CAA88921.1; -
DR EMBL; AD001528; AAB61308.1; -
DR EMBL; BC009898; AAH09898.1; -
DR PIR; S54160; S54160.
DR Genew; HGNC:11123; SMS.
DR MIM; 300105; -
DR GO; GO:0004766; F:spermidine synthase activity; TAS.
DR GO; GO:0006555; P:methionine metabolism; TAS.
DR GO; GO:0006595; P:polyamine metabolism; TAS.
DR InterPro; IPR001045; Sprmine_synthase.
DR Pfam; PF01564; Spermine_synth; 1.
DR PROSITE; PS01330; SPERMIDINE_SYNTHASE; 1.
KW Transferase.

FT DOMAIN 192 232 BINDING TO DECARBOXYLATED SAM (POTENTIAL).
FT CONFLICT 1 1 M -> MPG (IN REF. 1).
SQ SEQUENCE 366 AA; 41268 MW; D5B23EF61DE66443 CRC64;

Query Match 70.5%; Score 31; DB 1; Length 366;
Best Local Similarity 62.5%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|:|:|
Db 45 HGYLATYT 52

RESULT 13
SPSY_MOUSE STANDARD; PRT; 366 AA.
AC P97355;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Spermine synthase (EC 2.5.1.22) (Spermidine aminopropyltransferase) (SPMSY).
DE (SPMSY).
GN SMS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strom T.M., Francis F., Lorenz B., Boeddrich A., Econs M.J., Lehrach H., Meitinger T.;

RT "Pex gene deletions in Gy and Hyp mice provide mouse models for
RT X-linked hypophosphatemia."; submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RL [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Diaphragm;
RA Niiranen K., Korhonen V., Janne J.;
RT "Nucleotide sequence of mouse spermidine aminopropyltransferase
RT cDNA";
RL Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 316-366 FROM N.A.
RX MEDLINE=98133937; PubMed=9467015;
RA Lorenz B., Francis F., Gempel K., Boeddrich A., Josten M., Schmahl W.,
RA Schmidt J., Lehrach H., Meitinger T., Strom T.M.;
RT "Spermine deficiency in Gy mice caused by deletion of the spermine
RT synthase gene";
RL Hum. Mol. Genet. 7:541-547(1998).
CC -!- CATALYTIC ACTIVITY: S-adenosylmethionine + spermidine = 5'-
CC methylthioadenosine + spermine.
CC -!- PATHWAY: BIOSYNTHESIS OF SPERMINE FROM SPERMIDINE.
CC -!- SIMILARITY: BELONGS TO THE SPERMIDINE/SPERMINE SYNTHASES FAMILY.
CC
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CC
CC EMBL; Y09419; CAA70573.1; -.
DR EMBL; AF031486; AAB86631.1; -.
DR EMBL; AJ000093; CAA03919.1; -.
DR EMBL; AJ000087; CAA03918.1; -.
DR EMBL; AJ000088; CAA03918.1; JOINED.
DR EMBL; AJ000089; CAA03918.1; JOINED.
DR EMBL; AJ000090; CAA03918.1; JOINED.
DR EMBL; AJ000091; CAA03918.1; JOINED.
DR EMBL; AJ000092; CAA03918.1; JOINED.
DR MGD; MGI:109490; Sns.
DR GO; GO:0008215; P:spermine metabolism; IMP.
DR InterPro; IPR001045; Sprmine_synthase.
DR Pfam; PF01564; Spermine_synth; 1.
DR PROSITE; PS01330; SPERMIDINE_SYNTHASE; 1.
KW Transferase.
KW DOMAIN 192 232 BINDING TO DECARBOXYLATED SAM
FT (POTENTIAL).
FT SEQUENCE 366 AA; 41313 MW; D549F319F51C43C5 CRC64;
Query Match 70.5%; Score 31; DB 1; Length 366;
Best Local Similarity 62.5%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 HQYLSST 8
Db 45 HGYLATYT 52
RESULT 14
CGAL_CARAU STANDARD; PRT; 391 AA.
AC Q92161;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin A1 (Cyclin A).
GN CCNA1 OR CCNA.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=95377548; PubMed=7649388;
RA Katsu Y., Yamashita M., Hirai T., Tokumoto T., Kajiuura H.,
RA Nagahama Y.;
RT "Molecular cloning and immunological analysis of goldfish cyclin A
RT during oocyte maturation";
RL Dev. Biol. 170:616-625(1995).
CC -!- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF THE CELL CYCLE AT THE
CC G1/S (START) AND G2/M (MITOSIS) TRANSITIONS (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH THE CDK2 AND THE CDC2 PROTEIN KINASES TO
CC FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN
CC SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S79215; AAB35103.1; -.
DR HSP; P20248; IJSU.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Mitosis.
SQ SEQUENCE 391 AA; 43594 MW; 00402E02AFCB45F3 CRC64;
Query Match 70.5%; Score 31; DB 1; Length 391;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HQYLSST 8
Db 271 HQFLMQYT 278
RESULT 15
ATPA_CHLVU STANDARD; PRT; 506 AA.
AC P56294;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ATP synthase alpha chain (EC 3.6.3.14).
GN ATPA.
OS Chlorella vulgaris.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3077;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IAM C-27 / Tamiya;
RX MEDLINE=97303241; PubMed=9159184;
RA Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
RA Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,
RA Inamura A., Yoshinaga K., Sugiyama M.;
RT "Complete nucleotide sequence of the chloroplast genome from the
RT green alga Chlorella vulgaris: the existence of genes possibly
RT involved in chloroplast division".
RL Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY

```
CC SUBUNIT.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC H(+)(Out).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB001684; BAA57856.1; -
CC PIR; T07209; T07209.
CC InterPro; IPR000793; ATPase_a/bC.
CC InterPro; IPR000194; ATPase_a/bCentre.
CC InterPro; IPR004100; ATPase_a/bN.
CC InterPro; IPR000790; ATPase_ac.
CC InterPro; IPR005294; ATPsynthFl_alpha.
CC Pfam; PF00006; ATP-synt_ab; 1.
CC Pfam; PF00306; ATP-synt_ab_C; 1.
CC Pfam; PF02874; ATP-synt_ab_N; 1.
CC ProDom; PD001099; ATPase_ac; 1.
CC TIGRFAMs; TIGR00962; atpA; 1.
CC PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
KW ATP synthesis; Chloroplast; Thylakoid; Membrane; CF(1);
KW ATP-binding; Hydrolase; Hydrogen ion transport.
FT NP_BIND 170 177 ATP (POTENTIAL).
FT ACT_SITE 363 363 BY SIMILARITY.
SQ SEQUENCE 506 AA; 54708 MW; 47A292DB3907F4FB CRC64;

Query Match 70.5%; Score 31; DB 1; Length 506;
Best-Local Similarity 85.7%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYLSSYT 8
Db : 236 QYLSPYT 242
```

Search completed: August 13, 2003, 09:45:45
Job time : 26 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: August 13, 2003, 09:43:01 ; Search time 96 Seconds
(without alignments)
21.504 Million cell updates/sec

Title: US-10-056-052A-29
Perfect score: 44
Sequence: 1 HQYLSSYT 8
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 830525 seqs, 258052604 residues 830525
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Score		Match		Length		DB		ID		Description	
No.													
1	36	81.8	478	16	Q8F3B8.							Q8f3b8 leptospira	
2	35	79.5	181	11	Q99PN5							Q99pn5 mus musculu	
3	35	79.5	308	11	Q9CSC9							Q9csc9 mus musculu	
4	35	79.5	356	11	Q8CEE2							Q8cee2 mus musculu	
5	35	79.5	535	11	Q922Y3							Q922y3 mus musculu	
6	35	79.5	587	11	Q8R2Q0							Q8r2q0 mus musculu	
7	34	77.3	88	16	Q9PC98							Q9pc98 xylella fas	
8	34	77.3	281	5	Q8T8U4							Q8t8u4 drosophila	
9	34	77.3	468	16	Q9JVK7							Q9jvk7 neisseria m	
10	34	77.3	493	5	Q9BMU6							Q9bmu6 aedes aegyp	
11	34	77.3	543	5	Q8MQJ1							Q8mqj1 drosophila	
12	34	77.3	746	5	Q8INJ0							Q8inj0 drosophila	
13	34	77.3	1226	17	Q58836							Q58836 methanococc	
14	34	77.3	2531	5	O16004							O16004 lytechinus	
15	33	75.0	113	3	Q08428							Q08428 saccharomyc	
16	33	75.0	303	16	Q8DU06							Q8du06 streptococc	

17	33	75.0	404	5	Q9VN68	Q9vn68 drosophila
18	33	75.0	421	5	Q969A9	Q969a9 bombyx mori
19	33	75.0	462	16	Q9PKM4	Q9pkm4 chlamydia m
20	33	75.0	484	13	Q9W6F5	Q9w6f5 gallus gall
21	33	75.0	554	5	Q9U9I6	Q9u9i6 chrysops sp
22	33	75.0	557	5	Q8MTK0	Q8mtk0 choristoneu
23	33	75.0	590	13	Q9PTJ4	Q9ptj4 brachydanio
24	33	75.0	717	10	Q9FP07	Q9fp07 oryza sativ
25	33	75.0	730	5	Q20826	Q20826 caenorhabdi
26	33	75.0	796	16	Q8YZW1	Q8yzw1 anabaena sp
27	33	75.0	902	10	Q80455	Q80455 arabidopsis
28	33	75.0	902	10	P93831	P93831 arabidopsis
29	33	75.0	931	5	Q9VN69	Q9vn69 drosophila
30	33	75.0	931	10	Q8S4P6	Q8s4p6 zea mays (m
31	33	75.0	1015	10	Q8H2G7	Q8h2g7 oryza sativ
32	33	75.0	1121	3	Q9UUX7	Q9uux7 neurospora
33	33	75.0	1302	17	Q8TSC6	Q8tsc6 methanosarc
34	33	75.0	1304	17	Q8PVG7	Q8pvg7 methanosarc
35	33	75.0	1369	5	Q9VPW4	Q9vpw4 drosophila
36	33	75.0	1518	17	Q8THT8	Q8tht8 methanosarc
37	33	75.0	1733	17	Q8TTS9	Q8tts9 methanosarc
38	33	75.0	1845	17	Q8TTS7	Q8tts7 methanosarc
39	32	72.7	99	12	Q9Q0B0	Q9q0b0 anticarsia
40	32	72.7	102	13	Q9DDQ5	Q9ddq5 decapterus
41	32	72.7	102	13	Q9DDP9	Q9ddp9 decapterus
42	32	72.7	102	13	Q9DDQ4	Q9ddq4 decapterus
43	32	72.7	102	13	Q9DDQ0	Q9ddq0 decapterus
44	32	72.7	102	13	Q9DDQ1	Q9ddq1 decapterus
45	32	72.7	102	13	Q9DDQ3	Q9ddq3 decapterus

ALIGNMENTS

RESULT 1

Q8F3B8
ID Q8F3B8 PRELIMINARY; PRT; 478 AA.
AC Q8F3B8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Alginate O-acetylation protein.
GN LA2489.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiaceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Seroovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011416; AAN49688.1; -
KW Complete proteome.
SQ SEQUENCE 478 AA; 55633 MW; 745230B5BAD95BD1 CRC64;

Query Match 81.8%; Score 36; DB 16; Length 478;
Best Local Similarity 75.0%; Pred. NO. 40;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
||:|
Db 177 HQFLESYT 184

RESULT 2

Q99PN5
ID Q99PN5 PRELIMINARY; PRT; 181 AA.
AC Q99PN5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tripartite motif protein TRIM29 (Fragment).
GN TRIM29.

```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21231161; PubMed=11331580;
RA Raymond A., Meroni G., Fantozzi A., Merla G., Cairo S., Luzi L.,
RA Riganelli D., Zanaria E., Messali S., Cainarca S., Guffanti A.,
RA Minucci S., Pellicci P.G., Ballabio A.;
RT "The tripartite motif family identifies cell compartments.";
RL EMBO J. 20:2140-2151(2001).
DR EMBL; AF230390; AAG50169.1; -.
DR MGD; MGI:1919419; Trim29.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 20724 MW; 37B9F326AFEAAAC71 CRC64;

Query Match 79.5%; Score 35; DB 11; Length 181;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|:|:|
Db 110 HRYMNSYT 117

RESULT 3
Q9CSC9 Q9CSC9 PRELIMINARY; PRT; 308 AA.
AC Q9CSC9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 2810431N19Rik protein (Fragment).
GN TRIM29 OR 2810431N19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Suzuki R., Tomita M., Wagner L., Washio T.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Balzarelli R., Barsh G.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cdna collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK013219; BAB28721.1; -.
DR MGD; MGI:1919419; Trim29.
FT NON_TER 1
FT NON_TER 35316 MW; E7F6EB6C8414228C CRC64;
SQ SEQUENCE 308 AA; 35316 MW;

Query Match 79.5%; Score 35; DB 11; Length 308;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Suzuki R., Tomita M., Wagner L., Washio T.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Balzarelli R., Barsh G.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cdna collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK013219; BAB28721.1; -.
DR MGD; MGI:1919419; Trim29.
FT NON_TER 1
FT NON_TER 35316 MW; E7F6EB6C8414228C CRC64;
SQ SEQUENCE 308 AA; 35316 MW;

Query Match 79.5%; Score 35; DB 11; Length 308;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HQYLSSYT 8
|:|:|
Db 169 HRYMNSYT 176

RESULT 4
Q8CEE2 Q8CEE2 PRELIMINARY; PRT; 356 AA.
AC Q8CEE2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tripartite motif protein 29.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Skin;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK028448; BAC25956.1; -.
SQ SEQUENCE 356 AA; 40966 MW; 3A8E01AB7D1FAE28 CRC64;

Query Match 79.5%; Score 35; DB 11; Length 356;
Best Local Similarity 62.5%; Pred. No. 47;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|:|:|
Db 217 HRYMNSYT 224

RESULT 5
Q922Y3 Q922Y3 PRELIMINARY; PRT; 535 AA.
AC Q922Y3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Unknown (Protein for IMAGE:3498575) (Fragment).
GN TRIM29.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006699; AAH06699.1; -.
DR MGD; MGI:1919419; Trim29.
DR InterPro; IPR000315; Znf_Bbox.
DR Pfam; PF00643; zf-B_box; 1.
DR SMART; SM00336; BBOX; 2.
DR PROSITE; PS50119; zF_BBOX; 1.
FT NON_TER 1
FT NON_TER 535 AA; 60575 MW; 4D7081FCD39B7BAE CRC64;
SQ SEQUENCE 535 AA; 60575 MW;

Query Match 79.5%; Score 35; DB 11; Length 535;
Best Local Similarity 62.5%; Pred. No. 72;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
|:|:|
Db 396 HRYMNSYT 403
```

```
RESULT 6
Q8R2Q0
ID Q8R2Q0 PRELIMINARY; PRT; 587 AA.
AC Q8R2Q0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to tripartite motif-containing 29.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027353; AAH27353.1; -.
DR InterPro; IPR000315; Znf_Bbox.
DR Pfam; PF00643; zf-B_box; 1.
DR SMART; SM00336; BBOX; 2.
DR PROSITE; PS50119; ZF_BBOX; 1.
SQ SEQUENCE 587 AA; 65819 MW; D6E5C65F6A05EA98 CRC64;

Query Match 79.5%; Score 35; DB 11; Length 587;
Best Local Similarity 62.5%; Pred. No. 80;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
I:::|
Db 448 HRYMNSYT 455

RESULT 7
Q9PC98
ID Q9PC98 PRELIMINARY; PRT; 88 AA.
AC Q9PC98;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein xfl1883.
GN Xf1883.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RA Simpson A.J.G.; Reinach F.C.; Arruda P.; Abreu F.A.; Acencio M.;
RA Alvarenga R.; Alves L.M.C.; Araya J.E.; Baia G.S.; Baptista C.S.;
RA Barros M.H.; Bonaccorsi E.D.; Bordin S.; Bove J.M.; Briones M.R.S.;
RA Bueno M.R.P.; Camargo A.A.; Camargo L.E.A.; Carraro D.M.; Carrer H.;
RA Colauto N.B.; Colombo C.; Costa F.F.; Costa M.C.R.; Costa-Neto C.M.;
RA Coutinho L.L.; Cristofani M.; Dias-Neto E.; Docena C.; El-Dorri H.;
RA Facincani A.P.; Ferreira A.J.S.; Ferreira V.C.A.; Ferri J.A.;
RA Fraga J.S.; Franca S.C.; Franco M.C.; Frohme M.; Furlan L.R.;
RA Garnier M.; Goldman G.H.; Goldman M.H.S.; Gomes S.L.; Gruber A.;
RA Ho P.L.; Hohelsel J.D.; Junqueira M.L.; Kemper E.L.; Kitajima J.P.;
RA Krieger J.E.; Kuramae E.E.; Laigret F.; Lambais M.R.; Leite L.C.C.;
RA Lemos E.G.M.; Lemos M.V.F.; Lopes S.A.; Lopes C.R.; Machado J.A.;
RA Machado M.A.; Madeira A.M.B.N.; Madeira H.M.F.; Marino C.L.;
RA Marques M.V.; Martins E.A.L.; Martins E.M.F.; Matsukuma A.Y.;
RA Menck C.F.M.; Miracca E.C.; Miyaki C.Y.; Monteiro-Vitorello C.B.;
RA Moon D.H.; Nagai M.A.; Nascimento A.L.T.O.; Netto L.E.S.;
RA Nhani A. Jr.; Nobrega F.G.; Nunes L.R.; Oliveira M.A.;
RA de Oliveira M.C.; de Oliveira R.C.; Palmieri D.A.; Paris A.;
RA Peixoto B.R.; Pereira G.A.G.; Pereira H.A. Jr.; Pesquero J.B.;
RA Quaggio R.B.; Roberto P.G.; Rodrigues V.; de Rosa A.J.M.;
RA de Rosa V.E. Jr.; de Sa R.G.; Santelli R.V.; Sawasaki H.E.;
RA da Silva A.C.R.; da Silva A.M.; da Silva F.R.; Silva W.A. Jr.;
RA da Silveira J.F.; Silvestri M.L.Z.; Siqueira W.J.; de Souza A.A.;
RA de Souza A.P.; Terenzi M.E.; Truffi D.; Tsai S.M.; Tshako M.H.;
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RA Vallada H.; Van Sluys M.A.; Verjovski-Almeida S.; Vettore A.L.;
RA Zago M.A.; Zatz M.; Meidanis J.; Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE004008; AAF84689.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 88 AA; 9913 MW; 3EEAB9A47B358CAA CRC64;

Query Match 77.3%; Score 34; DB 16; Length 88;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
I:::|
Db 15 HQYISLST 22

RESULT 8
Q8T8U4
ID Q8T8U4 PRELIMINARY; PRT; 281 AA.
AC Q8T8U4; Q9VGA9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE AT29920p (CG11502 protein).
SV SVP OR CG11502 OR CG18158.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M.; Brokstein P.; Hong L.; Agbayani A.; Carlson J.;
RA Champe M.; Chavez C.; Dorsett V.; Dresnek D.; Farfan D.; Frise E.;
RA George R.; Gonzalez M.; Guarin H.; Kronmiller B.; Li P.; Liao G.;
RA Miranda A.; Mungall C.J.; Nunoo J.; Pacleb J.; Paragas V.; Park S.;
RA Patel S.; Phouanavong S.; Wan K.; Yu C.; Lewis S.E.; Rubin G.M.;
RA Celniker S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D.; Celniker S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.;
RA Amanatides P.G.; Scherer S.E.; Li P.W.; Hoskins R.A.; Galle R.F.;
RA George R.A.; Lewis S.E.; Richards S.; Ashburner M.; Henderson S.N.;
RA Sutton G.G.; Wortman J.R.; Yandell M.D.; Zhang Q.; Chen L.X.;
RA Brandon R.C.; Rogers Y.-H.C.; Blazej R.G.; Champe M.; Pfeiffer B.D.;
RA Wan K.H.; Doyle C.; Baxter E.G.; Helt G.; Nelson C.R.; Miklos G.L.G.;
RA Abril J.F.; Agbayani A.; An H.-J.; Andrews-Pfannkoch C.; Baldwin D.;
RA Ballew R.M.; Basu A.; Baxendale J.; Bayraktaroglu L.; Beasley E.M.;
RA Beeson K.Y.; Benos P.V.; Berman B.P.; Bhandari D.; Bolshakov S.;
RA Borkova D.; Botchan M.R.; Bouck J.; Brokstein P.; Brottier P.;
RA Burtis K.C.; Busam D.A.; Butler H.; Cadieu E.; Center A.; Chandra I.;
RA Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.;
RA de Pablos B.; Delcher A.; Deng Z.; Mays A.D.; Dew I.; Dietz S.M.;
RA Dodson K.; Doup L.E.; Downes M.; Dugan-Rocha S.; Dunkov B.C.; Dunn P.;
RA Durbin K.J.; Evangelista C.C.; Ferraz C.; Ferreira S.; Fleischmann W.;
RA Fosler C.; Gabrielian A.E.; Garg N.S.; Gelbart W.M.; Glasser K.;
RA Glodek A.; Gong F.; Gorrell J.H.; Gu Z.; Guan P.; Harris M.;
RA Harris N.L.; Harvey D.; Heiman T.J.; Hernandez J.R.; Houck J.;
RA Hostin D.; Houston K.A.; Howland T.J.; Wei M.-H.; Ibegwam C.;
RA Jalali M.; Kalush F.; Karpen G.H.; Ke Z.; Kennison J.A.; Ketchum K.A.;
RA Kimmel B.E.; Kodira C.D.; Kraft C.; Kravitz S.; Kulp D.; Lai Z.;
RA Lasko P.; Lei Y.; Levitsky A.A.; Li J.; Li Z.; Liang Y.; Lin X.;
RA Liu X.; Mattei B.; McIntosh T.C.; McLeod M.P.; McPherson D.;
RA Merkulov G.; Milshina N.V.; Mobarry C.; Morris J.; Moshrefi A.;
RA Mount S.M.; Moy M.; Murphy B.; Murphy L.; Muzny D.M.; Nelson D.L.;
RA Nelson D.R.; Nelson K.A.; Nixon K.; Nusskern D.R.; Pacleb J.M.;
RA Palazzolo M.; Pittman G.S.; Pan S.; Pollard J.; Puri V.; Reese M.G.;
RA Reinert K.; Remington K.; Saunders R.D.C.; Scheeler F.; Shen H.;
RA Shue B.C.; Siden-Kiamos I.; Simpson M.; Skupski M.P.; Smith T.;
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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferrieria S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanenvong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY075272; AAL68139.1; -
DR EMBL; AE003695; AAF54774.2; -
DR HSSP; P19793; 1LBD.
DR FlyBase; FBgn0003651; svp.
DR InterPro; IPR000536; Hormone_rec_lig.
DR Pfam; PF00104; hormone_rec; 1.
DR SMART; SM00430; HOLI; 1.
SQ SEQUENCE 281 AA; 31347 MW; F604481821AB7259 CRC64;

Query Match 77.3%; Score 34; DB 5; Length 281;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
Db 43 HSYLSSY 49

RESULT 9
Q9JVK7
ID Q9JVK7 PRELIMINARY; PRT; 468 AA.
AC Q9JVK7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE putative two-component system sensor kinase (EC 2.7.3.-).
GN NMA0797.
OS Neisseria meningitidis (serogroup A).

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.";
RL Nature 404:502-506(2000).
CC -!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
DR EMBL; AL162754; CAB84080.1; -
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003660; HAMP.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hiska; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
KW Kinase; Phosphorylation; Sensory transduction; Transferase;
KW Complete proteome.
SQ SEQUENCE 468 AA; 52804 MW; 47FD3A0BC67416B2 CRC64;

Query Match 77.3%; Score 34; DB 16; Length 468;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSYT 8
Db 93 HRYDSYT 100

RESULT 10
Q9BMU6
ID Q9BMU6 PRELIMINARY; PRT; 493 AA.
AC Q9BMU6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Nuclear hormone receptor.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhu J., Miura K., Dittmer N.T., Raikhel A.S.;
RT "A mosquito homolog of chicken ovalbumin upstream promoter transcription factor represses the 20-hydroecdysone response during vitellogenesis.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL; AF303224; AAG53940.1; -
DR HSSP; P19793; 2NLL.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Stdhrmn_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.

DR PRINTS; PR00047; STROIDFINGER.
DR ProDom: PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 493 AA; 54072 MW; 02AED5107CD2B45C CRC64;

Query Match 77.3%; Score 34; DB 5; Length 493;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
Db 255 HSYLSSY 261

RESULT 11

Q8MQJ1 PRELIMINARY; PRT; 543 AA.
Q8MQJ1;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE RE08410p.
GN SVP OR CG11502 OR CG18158.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL; AY129452; AAM76194.1; -.
DR FlyBase; FBgn0003651; svp.
DR InterPro; IPR000536; Hormone_rec_llg.
DR InterPro; IPR001723; Stdhrmn_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 543 AA; 58047 MW; DD04FD10042C2D3C CRC64;

Query Match 77.3%; Score 34; DB 5; Length 543;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
Db 305 HSYLSSY 311

RESULT 12

Q8INJ0 PRELIMINARY; PRT; 746 AA.
ID Q8INJ0
AC Q8INJ0;

DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CG11502-PA.
GN SVP.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rehnert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Wang X.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskaas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003695; AAN13541.1; -;
SQ SEQUENCE 746 AA; 76814 MW; D6085838A848087B CRC64;

Query Match 77.3%; Score 34; DB 5; Length 746;
Best Local Similarity 85.7%; Pred. NO. 1.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 HQYLSSY 7
| | | | |
305 HSYLSSY 311

RESULT 13
Q58836
ID Q58836 PRELIMINARY; PRT; 1226 AA.
AC Q58836;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein MJ1441.
GN MJ1441.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: STRONG TO P.DENITRIFICANS COBN AND M.JANNASCHII
CC MJ0907.
DR EMBL; U67585; AAB99452.1; -;
DR TIGR; MJ1441; -;
DR InterPro; IPR003672; CobN/Mg_chltase.
DR Pfam; PF02514; cobN-Mg_chel; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1226 AA; 141327 MW; 8F7DDF4E36162AB9 CRC64;

Query Match 77.3%; Score 34; DB 17; Length 1226;
Best Local Similarity 71.4%; Pred. NO. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HQYLSSY 7
| | | | |
Db 509 HQYIASY 515

RESULT 14
Q58836

OL6004
ID OL6004 PRELIMINARY; PRT; 2531 AA.
AC OL6004;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Notch homolog.
OS Lytechinus variegatus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Lytechinus.
OX NCBI_TaxID=7654;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97454256; PubMed=9310331;
RA Sherwood D.R., McClay D.R.;
RT "Identification and localization of a sea urchin Notch homolog:
RT insights into vegetal plate regionalization and Notch receptor
RT regulation.";
RL Development 124:3363-3374(1997).
DR EMBL; AF000634; AAB82088.1; -;
DR HSSP; P01132; 1EGF.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000800; Notch.
DR Pfam; PF00023; ank; 6.
DR Pfam; PF00008; EGF; 35.
DR Pfam; PF00066; notch; 3.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR00010; EGFLOOD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 5.
DR SMART; SM00179; EGF_CA; 23.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS50088; ANK_REPEAT; 5.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 21.
DR PROSITE; PS00022; EGF_1; 33.
DR PROSITE; PS01186; EGF_2; 25.
DR PROSITE; PS01187; EGF_CA; 20.
KW ANK repeat; EGF-like domain; Repeat.
SQ SEQUENCE 2531 AA; 273982 MW; 5BF42BEC627CA303 CRC64;

Query Match 77.3%; Score 34; DB 5; Length 2531;
Best Local Similarity 62.5%; Pred. NO. 6.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HQYLSSY 8
| | | | |
Db 949 HEYVDSY 956

RESULT 15
Q08428
ID Q08428 PRELIMINARY; PRT; 113 AA.
AC Q08428; O00018;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF YOR053W.
GN YOR053W OR YOR29-04.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 1-8 FROM N.A.
RA Landt O., Hiesel R., Unseld M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RA Bohn C., Bolotin-Fukuhara M., Daignan-Fornier B., Dang D.V.,
RA Valens M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97279235; PubMed=9133743;
RA Valens M., Bohn C., Daignan-Fornier B., Dang V., Bolotin-Fukuhara M.;
RT "The sequence of a 54.7 kb fragment of yeast chromosome XV reveals the
RT presence of two tRNAs and 24 new open reading frames.";
RL Yeast 13:379-390(1997).
DR EMBL; 274961; CAA99245.1; -;
DR EMBL; 270678; CAA94538.1; -;
DR SGD; S0005579; YOR053W.
RP SEQUENCE 113 AA; 15256 MW; D4841A26AA5FB64C CRC64;
Query Match 75.0%; Score 33; DB 3; Length 113;
Best Local Similarity 85.7%; Pred. NO. 35;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 HQYLSSY 7
Db 82 HQYRSSY 88

Search completed: August 13, 2003, 09:47:29
Job time : 99 secs

